```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

M protein - protein search, using sw model

August 6, 2002, 17:05:14 ; Search time 66.51 Seconds no un

(without alignments)
24.560 Million cell updates/sec

US-10-020-139-2_COPY_68_83 1 SSAWQLAKQKAQEAEKL 17

erfect score: coring table: edneuce:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 earched: 283138 otal number of hits satisfying chosen parameters:

inimum DB seq length: 0 aximum DB seq length: 2000000000

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

2: pir2:* 3: pir3:* 4: pir4:* 1: pir1:* 2: pir2:* 3: pir3:* PIR_71:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		escrip	valine-tRNA ligas	ptidase Clo	prot	- 03		a	penicillin amidase		outH protein - Erw	recept	hypothetical prote		d		iption	Ę	ical p	qp30	gp30	ţ	d hyp	septum formation m		divIB protein - Ba	0		cell division prot	II sec	2
		ID	7.1	D71711	B051	202	E71414	A26528	1 PNECA	D70437	S32862	AI0795	T46922	AC1981	C97707	S67564	D83270	S40766	T48814	AH1644	AI1358	T46199	AD0309	4	75	0.4	T18873	97	950	B.1	T48783
		DB	. 7	7	~	7	7	,	Н	7	7	7	~	~	~	7	~	7	~	7	7	7	~	7	7	7	~	7	7	7	~
		Length	· LO	S	~	∞	ω	4	4	ထ	ထ	\sim	0	4	S	σ	14	3	95	$^{\circ}$	125	S	7	σ	S	Ø	4	σ	σ	~	469
dР	Query	Match	7.8	'n,	i.	Ξ.	50.6	0	0	σ.	თ	σ.	თ		49.4		σ Ο	თ.		œ.	48.2	•	ω.	œ	œ.	œ.	•	œ	œ	ф С	
		Score	48	46	43	43	42	42	42	41	41	41	41	41	41	41	41		41	. 40	40	40	40	40	40	40	40	40		40	40
	esult	No.	1	7	m	4	ſΩ	9	7	œ	on.	10	11	12	13	14	15	16	17	18	19	20.	21	22	23	24	25	56	27	28	58

3 AWQLAKQKAQEAEK 16

δ

Millernate names: ATP-binding chain B - Rickettsia prowazekii
NiAlternate names: ATP-dependent Clp proteinase regulatory chain
NiAlternate names: ATP-dependent Clp proteinase regulatory chain
NiContains: adenosinetribiosophatase (EC 3.6.1.3)
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 19-Jan-2001
C;Accession: D71711
R;Andersson, S.G.E.: Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmar Nature 396, 133-140, 1998
A;Tile: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71630; MUID:99039499
A;Accession: D71711
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-858 <AND>
A;Residues: 1-858 <AND>
A;Residues: 1-858 <AND>
A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14507.1; PID:g38
A;Experimental source: strain Madrid E
C;Genetics:

W W W W W W W W W A 4 4 4 4 4 4 0 0 11 0 11 0 11 0 11 0 1	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4444444444444444 \$	578 629 629 632 633 715 715 7125 7125 7139 6439 685	0000000000000000	AG0119 AG0179 AG0179 AG1799 T02627 G75339 T75507 B86748 A594818 A594818 A594818 A5928 E81102 A81102 A81246 D83427	probable CmpA-fami probable exported GidA protein homol hypothetical prote probable exodeoxyr hypothetical prote DNA mismatch repai hypothetical prote myosin-vi [similar myosin-vi [similar myosin-vi [similar ranscription-repa transcription-repa glucan 1,4 alpha-g multiple ligand-bi methionyl-tRNA syn probable transcrip
RESULT 1 B71250 Valine-tRNA ligase (C.Species: Treponema	1 RNA 119 11 Trepo		EC 6.1.1.9) pallidum sub sequence_rev	.9) sus	(val sp. isic	S) - syphilis spirochete pallidum (syphilis spirochete) n 24-Jul-1998 #text_change 24-Nov-1999
R.Frasor, C.M.; Norris, S., rson, J.; Khalak, H.; Richthey, L.; Weidman, J.; Smi Science 281, 375-388, 1998 A.frle: Complete genome so A. Reference number: A71250	ission: B/1250 ier, C.M.; Norribur, Khalak, H.; Weidman, J.; Weidman, J.; e. 281, 375-388, e.: Complete gen trence number: Arence number: Arence particles of the complete gen for a com	Norris, Norris, (, H.; R in, J.; 5-388, 1 ce genom per: A71	S.J.; Weir ichardson, Smith, H.O. 998 e sequence 250; MUID:9	We SOr H.	is Milzon (C.M.: Morris, S.J.; Weinstock, G.M.; White Khalak, H.; Richardson, D.; Howell, J.K.; Weidman, J.; Smith, H.O.; Venter, J.C. (1, 375-388, 1998) omplete genome sequence of Treponema palli e number: A71250; MUID:98332770	S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Chardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Smith, H.O.; Venter, J.C. sequence of Treponema pallidum, the syphilis spirochete. Sequence of Treponema pallidum, the syphilis spirochete.
A; Accessi A; Status: A; Molecul A; Residue A; Cross-r A; Experim	on: B/J prelin e type: ss: 1-95 referenc	ninary; : DNA 56 <col/> ces: GB:	nuclei AE0012 strain	71;	A; Accession: B/1230 A; Status: preliminary; nucleic acid sequence A; Molecule type: DNA A; Residues: 1-956 <col/> A; Cross-references: GB: AE001271; GB: AE000520; A; Experimental source: strain Nichols	not shown; translation not shown; NID:g3323363; PIDN:AAC26589.1; PID:g33
A:Gene: TP1035 C:Superfamily: C:Keywords: ami Query Match	TP1035 : TP1035 : TP1035 : TP1035 ords: amin ords: amin	35 y: valinetRNA ligase aminoacyl-tRNA synthet th 57.8%:	tRNA liga RNA synth	iga inth inth 188;	synthetase; ligase; 7.8%; Score 48; D	ie; protein biosynthesis DB 2; Length 956;
Matches	3	Conservative	vat	1	3; Mismato	hes 3; Indels 0; Gaps 0;

ö

```
Cippedios: Arabidopsis thaliana (mouse-ear cress)
A.Variety: columbia
A.Variety: columbia
A.Variety: columbia
CiAccession: E71414
R.Beavan, M.: Bent, E.: Love, K.: Goodman, H.: Dean, C.: Bergkamp, R.: D
P.: Wedler, H.: Wedler, E.: Wambutt, R.: Weitzenegger, T.: Pohl, T.M.: Terryn, N.: G
avanagh, T.: Hempel, S.: Kotter, P.: Entian, K.D.: Rieger, M.: Schaeifer, M.: Funk, B
A.Authors: Mueller-Auer, S.: Silvey, M.: James, R.: Montfort, A.: Pons, A.: Puigdomen
A.Authors: Mueller-Auer, S.: Silvey, M.: James, R.: Montfort, A.: Pons, A.: Puigdomen
erhoft, A.: Moores, T.: Jones, J.D.G.: Eneva, T.: Palme, K.: Benes, V.: Rechman, S.:
C.: Chalwatzis, N
A.Reference number: A71400: MuID:9812113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Kluyvera cryocrescens
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A26528
R.Barbero, J.L.: Buesa, J.M.; Gonzalez de Buitrago, G.; Mendez, E.; Perez-Aranda, A.:
Gene 49, 69-80, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete nucleotide sequence of the penicillin acylase gene from Kluyvera ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-736 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: GB:297337; NID:92244829; PID:e327432; PID:92244865 C:Genetics:
                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: pac
C;Superfamily: penicillin amidase
C;Keywords: antibiotic resistance; hydrolase; penicillin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the authors translated the codon CAG for residue 719 as {\rm Glu} A;Note: the source is designated as Kluyvera citrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N, Alternate names: penicillin acylase; penicillin amidohydrolase
                                                                                                                                                                                                                                          Ouery Match 51.8%; Score 43; DB 2; Length 685; Best Local Similarity 63.6%; Pred. No. 63; Marches 7; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 42; DB 2; Length 736;
53.3%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                penicillin amidase (EC 3.5.1.11) – Kluyvera cryocrescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A26528; MUID: 87192002
                          A;Gene: metG; NNA0275
C;Superfamily: methionine--tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: ATCC 21285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:M15418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 SAWKLAKLNSNEATR 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SAWQLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 WELAKOEGODA 478
                                                                                                                                                                                                                                                                                                                                                                                                                       4 WULAKOKAQEA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 8: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-844 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A26528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                  Description: allows clop to hydrolyze polypeptides and proteins, probably by a chaperd activity. ATP hydrolyzis is required for Clp hydrolysis of proteins but not of smaller Superfamily: endopeptidase Clp ATP-binding chain keywords: ATP; hydrolase; molecular chaperone; nucleotide binding; P-loop 207-214/Region: nucleotide-binding motif A (P-loop) 604-611/Region: nucleotide-binding motif A (P-loop) 672-67/Region: nucleotide-binding motif B (P-loop) 877-867/Region: nucleotide-binding motif B (P-loop) 873-786/Gregion: nucleotide-binding motif B (P-loop) 873-786/Gregion: nucleotide-binding motif B (P-loop) 873-86/Region: nucleotide-binding motif B (P-loop) 672-67/Region: nucleotide-binding motif B (P-loop) 874-86/Gregion: nucleotide-binding predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uJ-like protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain Species: Salmonella enterica subsp. enterica serovar Typhi Note: this species has also been called Salmonella typhi Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Accession: AB0514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ichionine--tRNA ligase (EC 6.1.1.10) NMA0275 [imported] - Neisseria meningitidis (strai
Species: Neisseria meningitidis
Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AL162752; GB:AL157959; NID:97378778; PIDN:CAB83583.1; PID:9737903
Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
ture 413, 848-852, 2001
Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Atther: Complete genome sequence of a multiple drug resistant Salmonella enterica serov Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
1, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream.ture 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AL513382; PIDN:CAD01250.1; PID:q16501379; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.8%; Score 43; DB 2; Leugth 270; Best Local Similarity 66.7%; Pred. No. 25; Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 2; Length 858;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: djlA
Superfamily: dnaJ amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.4%; 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 NTKWQAEKSKLQQAQKL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 EMAKOKAQEIQK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QLAKQKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-270 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-685 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
Molecula type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: G82022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: G82022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: AB0514
Gene: clpB; RP036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

0

Gaps

```
ATITIE: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300, MUID:98196666
A,Racession: D70437
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Rolecule type: DNA
A,Residues: 1-185 cAQPA
A,Cross-references: GB.AE000746; NID:92983925; PIDN:AAC07478.1; PID:92983929; GB.AE0
A,Experimental source: strain VF5
A,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Erwina carcucovora
Cispecies: S31851, S31851, Wharam, S.; Gibson, M.; Allison, G.; Bunce, N.; Baral
Mol. Microbiol. 8, 443-456, 1993
A.Title: Molecular cloning and characterization of 13 out genes from Erwinia carctory
Dacteria.
A.Reference number: S32857; MUID:93316842
A.Recession. S32862
A.Status: preliminary: nucleic acid sequence not shown; translation not shown
A.Residues: 1-188 cREE>
A.Residues: 1-188 cREE>
A.Residues: 1-188 cREE>
A.Rote: the nucleotide sequence was submitted to the EMBL Data Library, /./
                                    A;Description: hydrolyzes penicillins G and V into fatty acid and 6-aminopenicillani. C;Superfamily: penicillin amidase
C;Keywords: antibiotic resistance; hydrolase; penicillin resistance
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-846/Product: penicillin amidase zymogen #status predicted <PRO>
F;290-846/Product: penicillin amidase heavy chain #status predicted <MPT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                 Length 846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 185
                                                                                                                                                                                                                                                                                                                                                                                        50.6%; Score 42; DB 1; Length 846
41.2%; Pred. No. 1.1e+02;
tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.4%; Score 41; DB 2; Best Local Similarity 72.7%; Pred. No. 36; Matches 8; Conservative 2; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 41; DB 2;
81.8%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP synthase FO subunit b - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Superfamily: secretion protein xcpU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outH protein - Erwinia carolovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 SNMWVIGKSKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 81.55
Conservative
9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AKKKAQEYEKL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AKOKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: outH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA (131-271,'A',273-631,'P',633-846 < COHS> (129,'T',131-271,'A',273-631,'P',633-846 < COHS> (129,'T',131-271,'A',273-631,'P',633-846 < COHS> (129,'T',131-271,'A',273-631,'P',633-846 < COHS> (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-61,1262) (131-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Title: Characterization of the regulatory region of the Escherichia coli penicillin ad ;Reference number: 154005; MUID:87219870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
| Residues: 1-67, R',69-76, R',78-96, S',98-129, T',131-216, G',218-341, L',343, WF',376
| Cross-references: GB:M11672; NID:9147044; PIDN:AAA24258.1; PID:9147047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Complete nucleotide sequence of the penicillin G acylase gene and the flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GR:W15950: NID:g147062; PIDN:AAA24269.1; PID:g147063; Slade, A.; Horrocks, A.J.; Lindsay, C.D.; Dunbar, B.; Virden, R. ur. J. Blochem. 197, 75-80, 1991; Title: Site-directed chemical conversion of serine to cysteine in penicillin acylase; Reference number: S15375; MUID:91200064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein
Residues: 27.36.291-299 <SLA>
Bruns, W.: Hoppe, J.: Tsai, H.; Bruening, H.J.: Maywald, F.; Collins, J.: Mayer, H.
Mol. Appl. Genet. 3, 36-44, 1985
Tille: Structure of the penicillin acylase gene from Escherichia coll: A periplasmic
Reference number: 156367; MuID:85236066
                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enicillin amidase (EC 3.5.1.11) precursor - Escherichia coli

Alternate names: penicillin G acylase: penicillin G amidohydrolase

Species: Escherichia coli

3Date: 30-Sep-1987 #sequence_revision 26-Jan-1996 #text_change 18-Jun-1999

Accession: A23593: S23375; A23983; 154005; S15375; 156367; 173437

Schumacher, G.; Sizmann, D.; Haug, H.; Buckel, P.; Bock, A.

ucleic Acids Res. 14, 5713-5727, 1986

7Title: Penicillin acylase from E. coli: unique gene-protein relation.

Reference number: A23593; MUID:86286584
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule_type: DNA
;Residues: 741-788,′Q′,790-846 <RE3>
;Cross-references: GB:M12373; NID:g147045; PIDN:AAA24259.1; PID:g147048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GB:X04114; NID:942247; PIDN:CAA27728.1; PID:942248; Oh. S.J.; Kim, Y.C.; Park, Y.W.; Min, S.Y.; Kim, I.S.; Kang, H.S. ene 56, 87-97, 1987
                                                                                                                                    .
0
                                    50.6%; Score 42; DB 1; Length 844; 41.2%; Pred. No. 1.1e+02; tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A23983
Molecule type: DNA
Residues: 1.102, R',104-271, A',273-304, R',306-368 < OLL>
Staterimental source: ATCC 11105
Valle, F.; Gosset, G.; Tenorio, B.; Oliver, G.; Bolivar, F. ene 50, 119-122, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Reference number: S23375; MUID:88056318;Accession: S23375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status : translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.22
Best Local Similarity 41.22
                                                                                                                                                                                                                  1 SSAWQLAKQKAQEAEKI, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-846 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
Residues: 1-20 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: I73437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: 154005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A23593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Function:
```

```
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Keference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Residues: 1-995 <PAU>
A,Cross-references: EMBL:274079; NID:91431009; PIDN:CAA98590.1; PID:e252986; PID:9143
A;Experimental source: strain $288C
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Titte: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A.Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                          A,Cross-references: GB:BA000019; PIDN:BAB73355.1; PID:g17130745; GSPDH:GN00179
A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE006914; PIDN: AAL02597,1; PID: q15619095; GSPUB: GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: hypothetical protein D2770
C;Species: Saccharcmyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Feb-2001
C;Accession: S67564
R;Paulin, L.; Saren, A.M.; Laamanen, P.
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 41; DB 2; Length 844; 58.3%; Pred. No. 1.6e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%; Score 41; DB 2; Length 857; 50.0%; Pred. No. 1.7e+02; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YDL031w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clpB protein [imported] . Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 4L
C;Keywords: ATP; nucleotide binding; P-loop
F;181-188/Region: nucleotide-binding motif A (P-loop)
F;284-289/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: clpB
C;Superfamily: endopeptidase Clp ATP-binding chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 WQAEKSKLQQTQKL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WULAKUKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 SWQLAQGKAEQA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AWQLAKQKAQEA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-844 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-857 <KUR>
                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Accession: C97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S67564
A; Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                         A;Gene: alr1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                  obable receptor/regulator protein STV2545 [imported] - Salmonella enterica subsp. ente Species: Salmonella enterica subsp. enterica serovar Typhi Note: this species has also been called Salmonella typhi Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Accession: A10795 Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J; Churcher, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gaora, P. Lure 413, 848-852, 2001 Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.; Tile: Complète genome sequence of a multiple drug resistant Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pothetical protein alr1398 [imported] - Anabaena sp. (strain PCC 7120)
Species: Anabaena sp.
Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
Accession: AC1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:AL513382; PIDN:CAD07547.1; PID:q16503539; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
Accession: T46922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: chemotaxis cheV protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S. bmitted to the Protein Sequence Database, February 2000 Reference number: 224138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

49.4%; Score 41; DB 2; Length 334;
Best Local Similarity 61.5%; Pred. No. 64;
Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.4%; Score 41; DB 2; Length 409; 50.0%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: adult testis; clone DKFZp434B1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pothetical protein DKFZp434B1612.1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:AL157436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 SAWELGKVKGLKLEEL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AWERIQQLAQEAE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AWQLAKQKAQEAE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserva
   2 SAWQLAKQKAQ 12
                                                              42 SAWQLARFQAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
Molecule type: DNA
Residues: 1-334 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-409 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: DKF2p434B1612.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: AI0795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T46922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: STY2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics
```

```
0; Gaps
                                                                                          Length 995;
                                                                                    Ouery Match 49.4%; Score 41; DB 2; Length 995; Best Local Similarity 69.2%; Pred. No. 1.9e+02; Matches 9; Conservative 2; Mismatches 2; Indels
;288-291/Region: DEAD motif
```

||||: | :|||| | 621 QLAKKTAMKAEKL 633 5 QLAKQKAQEAEKL 17

Ω

ranscription-repair coupling protein Mid PA3002 [imported] - Pseudomonas aeruginosa (st ;Species: Pseudomonas aeruginosa ;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

Accession: D83270 Security No. 1 Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br dman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, alure 406, 959-964, 2000 Security Security Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor Reference number: A82950; MUID:20437337

Status: preliminary Molecule type: DNA

Residues: 1-1148 <STO> \$Cross-references: GB:AE004725; GB:AE004091; NID:99949100; PIDN:AAG06390.1; GSPDB:GN001 \$Experimental source: strain PAO1 ;Superfamily: transcription-repair coupling protein :Gene: mfd; PA3002

0; Gaps Query Match 49.4%; Score 41; DB 2; Length 1148; Best Local Similarity 61.5%; Pred. No. 2.2e+02; Matches 8; Conservative 1; Mismatches 4; Indels

0

earch completed: August 6, 2002, 17:05:15 ob time: 917 sec í II II:II i 548 SETWQKAKRKAAE 560

1 SSAWQLAKQKAQE 13

```
(without alignments)
20.019 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      083998 treponema p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erwinia car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatitis d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methanococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methanococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          moraxella b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treponema p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kluyvera ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erwinia chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 campylobact
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                    August 6, 2002, 17:07:34 ; Search time 32.88 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P17999 e Q47112 e P04419 e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q58242
P18000
P57986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09ppb8
P39755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P31587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9k8h3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09k8a0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  093624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P09882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       083873
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACSU
                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPH_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AANT_HDVS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DJLA ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MORBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPOZ_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DBPA_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HDVS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEAST
                                                                                                                   US-10-020-139-2_COPY_68_84
                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                            1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEA8
                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 08
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                       SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                             Sequence:
                                                                        Run on:
                                                                                                                      ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
9
```

P09883 escherichia	P43828 haemophilus	P57838 pasteurella	P57972 pasteurella	Q9yfzl aeropyrum p	004932 craterostig	Q9vfb7 drosophila	P09790 neisseria g	Q64399 cricetulus	Q64511 mus musculu	Q02880 homo sapien	042131 gallus gall
CEA9_ECOLI	SYM_HAEIN	SYM_PASMU	MUTS_PASMU	RASO_AERPE	SPS1_CRAPL	Y623_DROME	IGA_NE1GO	TP2B_CRILO	TP2B_MOUSE	TP2B_HUMAN	TP2B_CHICK
-	-	Н	,	,-	-4	٦	٦	-	П		-
582	682	682	860	919	1054	1145	1532	1612	1612	1626	1627
45.8	45.8	45.8	45.8	45.8	45.8	45.8	45.8	45.8	45.B	45.8	45.8
3.8	38	38	38	38	38	38	38	38	38	38	38
34	35	36	37	38	6£	40	4.1	42	43	44	45

ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Duropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            AEDLINE=9833270; PubMed-9665876; AETAIN-NICHOLS; MEDLINE=9833270; PubMed-9665876; AETAIN-NOTIS S.J., Weinslock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujil C., Garland S., Wenter B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Science 281:375-388(1998).
-!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) - AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: CYLOPIASMIC.
-1- SUBCELLULAR LOCATION: CYLOPIASMIC.
-1- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                       15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Valy1-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
VALS OR TP1035.
                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "KMSKS" REGION.
ATP (BY SIMILARITY).
1; 7D50583C7C6BA35A CRC64;
                                                                                                                                        Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                 956 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interpro; IPR002300; tRNA-synt_la.
Interpro; IPR001412; tRNA-synt_l.
Interpro; IPR002303; tRNA-synt_val.
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107362 MW;
                                                   15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001271; AAC26589.1; -.
HSSP; P96142; 1GAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00133; tRNA-synt_1; 1
PRINTS; PR00986; TRNASYNTHVAL
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-valy1-tRNA(Val).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
570
569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566
569
956 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TP1035;
                 SYV_TREPA
083998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
SYV_TREPA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A BETA CHAIN.
SUBCELLLAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S45 (SERINE PROTEASE) ALSO
KNOWN AS THE PENICILLIN ACYLASE FAMILY.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92109664; PubMed=1764029;
Martin J., Slade A., Aitken A., Arche R., Virden R.;
"Chemical modification of serine at the active site of penicillin acylase from Kluyvera citrophila.";
Biochem. J. 280:659-662[1931].
-!- CATALYTIC ACTIVITY: Penicillin + H(2)0 = a fatty acid anion + 6-
                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbero J.L., Buesa J.M., de Bultrago G.G., Mendez E., Perez-Aranda A., Carcia J.L., "Complete nuclectide sequence of the penicillin acylase gene from Kluyvera citrophila.";
                                                                                                                                                                                                                                                                                                                                       Kluyvera citrophila (Kluyvera cryocrescens).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENICILLIN G ACYLASE ZYMOGEN,
PENICILLIN G ACYLASE ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR002692, Penicil_amidase.
Pfam, PF01804, Penicil_amidase, 1.
Hydrolase, Antiblotic resistance: 2ymogen, Periplasmic; Signal.
                                       .,
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENICILLIN G ACYLASE BETA SUBUNIT
57.8%; Score 48; DB 1; Length 956; 57.1%; Pred. No. 6.2; 1.1%; Pred. No. 6.2; 1.1% Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3466059B0FC4E5AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPACER PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 290-297, AND ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 21285;
MEDLINE=87192002; PubMed-3032748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M15418; AAA25047.1; -.
                                                                                                                                                                                                                                                                                                   (Penicillin amidohydrolase)
                                     Conservative
                                                                                                                                                                                             STANDARD;
                                                                                                      892 AWOKAROKVOOVER 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
289
844
290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aminopenicillanate.
                                                                      3 AWQLAKQKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A26528; A26528.
HSSP; P06875; 1AJQ.
                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 49:69-80(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
290
290
844 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S45.001;
                                                                                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=580;
                                                                                                                                                                                           PAC_KLUC1
   Query Match
                                                                                                                                                                                                                                                                                                                                                                           Kluyvera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                         >-
                                                                                                      ō
```

Score 42; DB 1; Length 844; Pred. No. 47;

41.28;

Best Local Similarity

Query Match

```
ô
 Gaps
                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicilin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ob S.-J., Kim Y.-C., Park Y.-W., Min S.-Y., Kim I.-S., Kang H.-S.; "Complete nucleotide sequence of the penicillin G acylase gene and the flanking regions, and its expression in Escherichia coli."; Gene 56:87-97(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A common precursor for the two subunits of the penicillin acylase from Escherichia coli ATCC11105.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87219870; PubMed-3556321; Malle F., Gosset G., Tenorio B., Oliver G., Bolivar F.; "Characterization of the regulatory region of the Escherichia coli penicillin acytase structural gene.";
                                                                                                                                                                                                                                                                                                                                                                                                     Schumacher G., Sizmann D., Haug H., Buckel P., Boeck A.; "Penicillin acylase from E. coli: unique gene-protein relation."; Nucleic Acids Res. 14:5713-5727(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-AFCC 11105;
MEDILINE-66137424; PubMed*3005131;
Oliver G., Valle F., Rosetti F., Gomez-Pedrozo M., Santamaria P.,
Gosset G., Bolivar F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transcriptional and gene fusion analyses of the Escherichia coli
                                                                                                                                                                                                                                                                                                      Bacteria; Proleobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Penicillin acylase has a single-amino-acid catalytic centre.";
Nature 373:264-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 11105;
MEDLINE-95115804; Pubmed+7815145;
Dugqleby H.J., Tolley S.P., Hill C.P., Dodson E.J., Dodson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sizmann D., Keilmann C., Boeck A.; "Primary structure requirements for the maturation in vivo of penicillin acylase from Escherichia coli ATCC 11105.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radoja S., Francetic O., Stojicevic N., Moric I., Glisin S.,
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               penicillin amidase gene expression.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
٠,
                                                                                                                                                    846 AA.
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 192:143-151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-88056318; PubMed-3315861;
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86286584; PubMed=3016663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90382435; PubMed=2205499;
                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                   (Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-368 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-368 FROM N.A.
                                                            290 SNMWVIGKNKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-95 FROM N.A.
                                1 SSAWQLAKOKAQEAEKL 17
7; Conservative
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 50:119-122(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 40:9-14(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konstantinovic M.;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 11105;
                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                             PAC_ECOL1
P06875:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATURATION
Matches
                                                                                                                                 PAC_ECOLI
                                  δ
                                                                QQ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institutions the area are or restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                           -!- SUBBUTT: HETERODIMER OF AN ALPHA CHAIN AND A BETA CHAIN.
-!- SUBCELLUIAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S45 (SERINE PROTEASE) ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
CATALYTIC ACTIVITY: Penicillin + H(2)0 = a fatty acid anion + 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENICILLIN G ACYLASE ZYMOGEN, PENICILLIN G ACYLASE ALPHA SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01804; Penicil_amidase; 1.
Hydrolase; Antibiotic resistance; Zymogen; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENICILLIN G ACYLASE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)
(Transcriptase omega chain) (RNA polymerase omega subunit).
RPOZ OR SPY1630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%; Score 42; DB 1; Length 846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S->C: LOSS OF ACTIVITY.
A -> R (IN REF. 3).
I -> T (IN REF. 3).
R -> P (IN REF. 3).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
G -> P (IN REF. 2).
G -> P (IN REF. 2).
W; 48570EDC853BA227 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPACER PEPTIDE
                                                                            KNOWN AS THE PENICILLIN ACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002692; Penicil_amidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                       AF109125; AAD19653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94642 MW;
                                                                                                                                                                                                                                         X04114; CAA27728.1; -. M17609; AAA24324.1; -. M14424; AAA24270.1; -.
                                                                                                                                                                                                                            EMBL; M15950; AAA24269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 SNMWVIGKSKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSAWQLAKOKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                 aminopenicillanate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
846
235
235
289
289
290
290
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                          1AJN; 12-NOV-97.
1AJP; 12-NOV-97.
                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-97
                                                                                                                                                                                                                                                                                                                                                    16-MAR-96
                                                                                                                                                                                                                                                                                                                                                                                12-NOV-97
                                                                                                                                                                                                                                                                                                                                                                   12-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 AA;
                                                                                                                                                                                                                                                                                                         PNECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S45.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPOZ_STRPY
P82577;
                                                                                                                                                                                                                                                                                                                                                    1 PNM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPOZ_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute or there are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, I BETA' CHAIN AND I OMEGA CHAIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE RNA POLYMERASE OMEGA CHAIN FAMILY.
                                                                                                                Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clitton S.W., Roe B.A., McLaughlin R.Kreptococcus pyogenes."; "Complete genome sequence of an MI strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reeves P.J., Whitcombe D., Wharam S., Gibson M., Allison G., Bunce N., Barallon R., Douglas P., Mulholland V., Stevens S., Walker S.,
                                                                                                                                                                                                                                                                                             Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J., VanBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Promotes RNA polymerase assembly. Latches the N and C-terminal regions of the beta subunit thereby facilitating its interaction with the beta and alpha subunits (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                       'Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
General secretion pathway protein H precursor (Pectic enzymes secretion protein outH).
                                                                                                                                                                                                                                                           SEQUENCE OF 27-42; 46-60 AND 97-104, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 41; DB 1; Length 104; 53.8%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 AA; 11705 MW; FD6FDF3D852CC7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                         STRAIN=SF370 / ATCC 700294 / Serotype MI;
MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93316842; PubMed=8326859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006594; AAK34401.1; -
                                                                                                                                                                                                                                                                          STRAIN-JRS4 / Serotype M6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 53...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 QIAKEKEEEGEKI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ULAKUKAUEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                           SEQUENCE FROM N.A.
                       NCB1_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                              proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPH_ERWCA
P31587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPH_ERWCA
a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license effectment (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                     ************************
          "Molecular cloning and characterization of 13 out genes from Erwinia carotovora subspecies carotovora: genes encoding members of a general secretion pathway (GSP) widespread in Gram-negative bacteria."; Mol. Microbiol. 8:443-456(1993).

-i- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28:2315-2323(2000).
-!- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE. PROBABLY INTERACTS
WITH 60S RIBOSOMAL SUBUNIT. INVOLVED IN THE MATURATION OF 25S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burger F., Daugeron M.-C., Linder P., "Dbpl0p, a putative RNA helicase from Saccharomyces cerevisiae, is required for ribosome biogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL SECRETION PATHWAY PROTEIN H. METHYLATION (BY SIMILARITY). 733E90BFDDD6C5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycola; Saccharomycolina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! . SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-! - SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. HIGHLY SIMILAR TO S.POMBE SPAC31A2.07C.
                                                                                                                                 MULTIPLE PECTIC ENZYMES.
-:- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Probable RNA-dependent helicase DBP10 (DEAD-box protein 10).
DBP10 OR YDL031W OR D2770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 41; DB 1; Length 188; 72.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paulin L., Saren A.M.;
Submitted (APR-1996) to the EMBL/GenBank/DUBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        995 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO01120; Prok_N_methyltn.
PRINTS; PR00885; BCTERIALGSPH.
PROSITE; PS00409; PROKAR_NTER_METHYL; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE-20330350; PubMed-10871363;
                                                                                                                                                                                                                                                                                                                                                                       PIR, S31751; S31751.
PIR, S32862; S32862.
InterPro; IPR002416; Bac_GSPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 188 AA; 21390 MW;
                                                                                                                                                                                                                                                                                                                                                    EMBL; X70049; CAA49649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 72.79
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SAWQLAKQKAQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 SAWOLARFOAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIBOSOMAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
Salmond G.P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DBPA_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BPA_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ
₹₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₩₩₩₩₩₽₽₽₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B D E E E B N S O O X N D D S J N D X A E E J D D D D D D D
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson K., Ainscough K., Anderson K., Baynes C., Berks M., Bonfield J., Hurton J., Connell M., Copsey T., Cooper J., Coulson A., Erastra M., Derar S., Du Z., Durbin R., Favello A., Fraser A., Frastra M., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Klisten T., Lilier L., Jier M., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudan K., Watchan K., Watchan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2 Mb of contiguous nucleotide sequence from chromosome 111 of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 49.4%; Score 41; DB 1; Length 995; Best Local Similarity 69.2%; Pred. No. 78; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 134.9 kDa protein ZK512.5 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   995 AA; 113157 MW; 9AFA74D0BAB198A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; RNA-binding; Helicase; Nuclear protein. NP_BIND 181 188 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEAD_ATP_helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAD BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z74079; CAA98590.1; -. SGD; S0002189; DBP10. InterPro; IPR001410; DEAD. InterPro; IPR000629; DEAD.ATP_he InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00270; DEAD: 1.
Pfam: PF00271; helicase_C: 1.
SMART; SM00487; DEXUC: 1.
SMART: SM00490; HELICC: 1.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 271781; CAA96458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 QLAKKTAMKAEKL 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOQ5_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOU5_CAEEL
          SOUTH TERMINATION OF THE PRESENCE OF THE PRESE
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                  0
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
O
                                                                              Score 41; DB 1; Length 1232;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.2%; Score 40; DB 1; Length 190; Best Local Similarity 66.7%; Pred. No. 23; Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                                2; Indels
                                                1232 AA; 134923 MW; 6DFC35D664AA8D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A810954296FBE099 CRC64;
                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                           01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                          190 AA.
                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                         STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP001517; BAB06752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE 33 33 S1 PASEQUENCE 190 AA; 21240 MW;
                                                                                                                                                                                                                                          Septum formation protein Maf.
                                                                              49.48;
         EMBL; Z22177; CAA80146.1; -.
          ... squ/66; S40766.
WormPep; ZK512.5; CE00411.
Hypothetical profess
SEGNERAL
                                                                    Ouery Match
Best Local Similarity 53,500
Local Similarity 54,500
Local Similarity 54,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR003697; Maf. Pfam; PF02545; Maf; 1
                                                                                                                                        326 AYEKARQEAAESEKL 340
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                     3 AWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 QLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 QLARQKAQDVAK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=86665;
                                                                                                                                                                                                                                                      OR BH3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKL1_CAEEL
ID YKL1_CAEEL
                                                                                                                                                                                           MAF_BACHD
                                                                                                                                                                                MAF_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                        q
                                                                                                                                                                                                    qq
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C-125 / JCM 9153;
MEDLINE-20151288: PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative casein kinase 1 C03CI0.1 in chromosome III (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.2%; Score 40; DB 1; Length 341; 50.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
17AD6E173551BABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                    Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39037 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z35637; CAA84685.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; C03C10.1; CE00872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
45
135
                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 WIMEKOKAQOSO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTS2 OR BH3106.
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Loc 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WQI,AKQKAQEAE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q06486; 1CKI.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MutS2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS2_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Berks M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS2_BACHD
```

```
VARIANT DFNA22 TYR-442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYO6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sec http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avraham K.B., Hasson T., Sobe T., Balsara B., Testa J.R., Skvorak A.B., Morton C.C., Copeland N.G., Jenkins N.A.; "Characterization of unconventional MYO6, the human homologue of the responsible for deafness in Snell's waltzer mice."; Hum. Mol. Genet. 6:1225-1231(1997).
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wells A.L., Lin A.W., Chen L.-Q., Safer D., Cain S.M., Hasson T., Carragher B.O., Milligan R.A., Sweeney H.L.; "Myosin VI is an actin-based motor that moves backwards.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vortebrala, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                         48.2%; Score 40; DB 1; Length 785; 50.0%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                    PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; FALSE_NEG.
ATP-binding; DNA-binding; Complete proteome.
335 ATP ATP (POTEMTIAL).
SEQUENCE 785 AA: 87426 MW; DBED779F2F4671C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1262 AA.
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99447046; PubMed=10519557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97402203; PubMed=9259267;
                                                                                                                                                                     EMBL; AP001517; BAB06825.1; -. InterPro; IPR000432; MutS_C. InterPro; IPR002863; MutS_N. InterPro; IPR002625; Smr. Pfam; PF00488; MutS_C; 1. Pfam; PF00488; MutS_C; 1.
                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                          ProDom; PD001263; MutS_C; 1.
                                                                                                                                                                                                                                                    SMART; SM00534; MUTSac; 1
SMART; SM00533; MUTSd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            535 SDWEEAEKALQEAEOL 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 401:505-508(1999).
[4]
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       2 SAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                             SMART; SM00463; SMR;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
 Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avraham K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYO6_HUMAN
Q9UM54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYO6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVEEEEZ800×2844663284328344632
 ◆FEHODODODODEKKKKKKKKKKKKKKKKKKKKFF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                 -i- FUNCTION: RECESSIVE ACTIN-BASED MOTOR. REQUIRED FOR STRUCTURAL INTEGRATY OF INNER EAR HAIR CELLS (BY SIMILARITY).
-i- DISEASE: Defects in MYO6 are the cause of an autosomal dominant form of nonsyndromic sensorineural deafness (DFNA22). The deafness is progressive and postlingual, with onset during childhood (8 to 10 years of age at onset of symptoms; 6 to 8 years of age at onset of first audiometric abnormalities). By the age of approximately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
MEDLINE-1375573; PubMed-11468689; Melchionda S., Ahituv N., Bisceglia L., Sobe T., Glaser F., Rabionet R., Arbones M.L., Notarangelo A., Di Iorio E., Carella M., Estivill X., Avraham K.B., Gasparini P.; "MYO6, the human homologue of the gene responsible for deafness in Snell's waltzer mice, is mutated in autosomal dominant nonsyndromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 years, affected individuals invariably have profound sensorineural deafness.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.2%; Score 40; DB 1; Length 1262; 56.2%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTIG-VAR_012110.
1262 AA; 146047 MW; CPIFA35796FC1C60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTIE; PS50096; TQ; FALSE_NEG.
MYOSIN; ATP-binding; Calmodulin_binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
C -> Y (IN DFNA22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MY06_MOUSE STANDARD; PRT; 1265 AA. 064331; 16-0CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.4e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coiled coil; Disease mutation; Deafness
                                                                                                                                                                                                                       Genet. 69:635-640(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001609; IQ.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U90236; AAC51654.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 SALOKKKOOEEEAERL 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834
1030
158
672
442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
665
442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 600970; -
MIM; 606346; -
                                                                                                                                                                                                hearing loss.
                                                                                                                                                                                                                             Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYOG OR SV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

```
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ISOLATE JAPANESE S-1;
MEDLINE=91012805; PubMed=2214027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L02214; AAA24835.1; -.
                                                                                                                                                                                                                                                                                          SEQUENCE OF 85-181 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M37886; AAA24826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MULTIPLE PECTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                           Lindeberg M., Collmer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10427, 10421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fransport; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A37874; A37874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SAWQLAKOKAO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Deltavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SGWQIARFKAQ 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                        SEQUENCE FROM N.A
                       Pectobacterium.
NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delta antigen.
                                                                                                                                                                                                                                                                                                                    STRAIN-EC16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AANT_HDVS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  milieu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P25883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTT DDT DTT DDT T DT T DTT T D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or sond an email to license@isbs.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                              TISSUE-Brain;
BEDLINE-9608382; PubMed-7493015;
Avraham K.B., Hasson T., Steel K.P., Kingsley D.M., Russell L.B.,
Mooseker M.S., Copeland N.G., Jenkins N.A.;
The mouse Snell's waltzer deafness gene encodes an unconventional
myosin required for structural integrity of inner ear hair cells.";
Nat. Genet. 11:369-375(1995).
                                                                                                                                                                                                                                                                                                                                                                                  CONDITION CHARACTERIZED BY CIRCLING, HEAD-TOSSING, DEAFNESS AND
                                                                                                                                                                                                                                                               INTEGRITY OF INNER EARTH HAIR CELLS (BY SIMILARITY)

-1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITHIN THE CICHLEA,

EXPRESSED SPECIFICALLY WITHIN THE CELLS.

-1- DISEASE: DEFECTS IN MYOG ARE THE CAUSE OF SNELL'S WALTZER, A
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR 1992 (Rel. 21, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
General secretion pathway protein H precursor (Pectic enzymes secretion protein outH).
                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-i- SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.2%; Score 40; DB 1; Length 1265; 56.2%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN SNELL'S WALTZER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.4e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50096; IQ; FALSE_NEG.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation; Deafness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dOD; MGI:104785; Myo6.
Interpro; IPR000048; IQ.
Interpro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SMO015; 10; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146408 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myosin_head; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U49739; AAB00194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    914 SALQKKKQQEEEAERL 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00612, IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         led coil; Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          HYPERACTIVITY
                                           NCB1_Tax1D=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPH_ERWCH
P24687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSPH_ERWCH

ID GSPH_ER

P P24687

DT 01-MAR

DT 01-JUL

DE GENERAL

GROOT 01-JUL

DE GENERAL

GROOT 01-JUL

DE GENERAL

GROOT 01-JUL

OS ECTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
  δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the informatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                          "Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi: sequence comparison with secretion genes from other Gram-negative bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 selectively secrete a diverse family of heterologous proteins to its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 88:1079-1083(1991).
-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                       He S.Y., Lindeberg M., Chatterjee A.K., Collmer A.; "Cloned Erwinia chrysanthemi out genes enable Escherichia coli to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL SECRETION PATHWAY PROTEIN H. METHYLATION (BY SIMILARITY).
7E72A931042B63B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.0%; Score 39; DB 1; Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis delta virus (isolate Japanese S-1) (HDV), and Hepatitis delta virus (isolate 7/18/83) (HDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 31;
2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002416; Bac_GSPH.
InterPro; IPR001120; Prok_N_methyltn.
PRINTS; PR00885; BCTERIALGSPH.
PROSITE; PS00409; PROKAR_NTER_METHYL; I.
                                                                                                                                                                                             Bacteriol. 174:7385-7397(1992).
MEDLINE-93054355; PubMed-1429461;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91126059; PubMed~1992458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 181 AA; 20288 MW;
```

ó

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institution. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                              between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                    -t- DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC HEPATITIS DELTA VIRAL INFECTIONS.
-t- MISCELLANEOUS: DELTA ANTIGEN BINDS SPECIFICALLY TO HDV KNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Imazeki F., Omata M., Ohto M.;
"Heterogeneity and evolution rates of delta virus RNA sequences.";
J. Virol. 64:5594-5599(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imazeki F., Omata M., Ohto M.;
"Heterogeneity and evolution rates of delta virus RNA sequences.";
J. Virol. 64:5594-5599(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: DELTA ANTIGEN BINDS SPECIFICALLY TO HDV RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.0%; Score 39; DB 1; Length 195; 53.8%; Pred. No. 33; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR002506; HDV_ag.
Pfam: PF01517; HDV_ag; 1.
Probon: PD002887; HDV_ag; 1.
Antigen: RNA-binding: Nuclear protein; Phosphorylation.
SEQUENCE 195 AA; 21928 MW: E40EE957E032C20A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Delta annigen.
Hepatitis delta virus (isolate Japanese S-2) (HDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPATITIS DELTA VIRAL INFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91012805; Pubmed-2214027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90192; BAA14216.1; -. EMBL; X60193; CAA42749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.00
Best Local Similarity 53.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                   PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 WOLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 WITARKKAEELEK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ruses; Deltavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B36409; SAVLDS,
PIR; S18678; S18678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AANT_HDVS2
  Ω
```

```
CC or send an email to license@isb-sib.ch).

CC DR EMBL: D90(393; BAA14277.1; -
DR InterPro: JPR002506: HDV_ag.
DR Pidam; PF01517; HDV_ag.
DR Probom: P0002887: HDV_ag.
DR Probom: P0002887: HDV_ag.
DR Antigen: RNA-binding: Nuclear protein: Phosphorylation.
SQ SEQUENCE 195 AA: 21912 MW: D3C543267E9CA780 CRC64;
SQ SEQUENCE 195 AA: 21912 MW: D3C543267E9CA780 CRC64;
SQ SEQUENCE 195 AA: 21912 MW: D3C543267E9CA780 CRC64;

Query Match
SA: Pred. No. 33; Mismatches 3; Indels 0: Gaps 0;

QY 4 WOLAKCKAQEAEK 16
Db 21 WITARKKAEELEK 33

Search completed: August 6, 2002, 17:07:35

Job Lime: 877 sec
```

Page 9

```
Quets homo saplen
Qunkl homo saplen
Q9unkl homo saplen
Q9unk2 homo saplen
Q9unk2 homo saplen
Q9ung5 opsanus bet
Q9GQV8 mus musculu
Q9Jwp0 neisseria m
Q9LJ94 bacteriopha
Q6C253 escherichia
Q9Tvg0 tetrahymena
Q23362 arabidopsis
Q9vru6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9zea9 ricketīsia
Q94bī0 arabidopsis
                                                                   August 6, 2002, 17:09:29 ; Search time 111.35 Seconds (without alignments) 26.411 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96dr5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                         562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                )M protein - protein search, using sw model
                                                                                                                    US-10-020-139-2_COPY_68_84
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _092EA9
094BT0
09UET5
                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 4 096000
249 4 0960R5
858 16 0960R5
1043 10 0948T0
11220 4 0910ET5
1721 4 095216
1721 4 095016
1721 1 095000
124 1 095000
125 1 090000
685 16 090000
125 9 060253
731 5 096000
731 1 095000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       095216
Q9UNK2
Q9PUQ5
Q9D0Y8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9JWP0
                                                                                                                                                   1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                             1: Sp_archea:*
2: sp_bacteria:*
3: sp_fung!:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                  4inimum DB seq length: 0
4aximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                       SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               sb_mhc:*
                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fitle: .
                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                        Jatabase :
                                                                                                                                                   sednence:
                                                                                                                                                                                                                 searched:
                                                                          du on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lesult
```

095519 homo sapien 095742 leishmania 095712 lead mays (m 067526 aquifex aec 09c031 homo sapien 09c032 homo sapien 09c033 homo sapien 09c033 homo sapien 09h1b4 homo sapien 09h1b4 homo sapien 09h1b5 homo sapien 09h1b6 homo sapien 09h1b6 homo sapien 09h1b6 mano sapien 09h1b6 homo sapien 09h1b6 mano sapien 09c035 homo sapien 09f035 homo sapien 09f036 homo sapien 09f036 arabidopsis 09f240 homo sapien 09f164 arabidopsis 09f241 neurospora 09258 listeria in 066724 equine infe 09smp3 arabidopsis 09f12 actinobacil 09f280 actinobacil	ALIGNMENTS PRT; 249 AA. 17, Created) 17, Last sequence update) 19, Last annotation update) 19, Last annotation update) VINE SALIVARY PROTEIN BSP30). data; Craniata; Vertebrata; Euteleostomi; ates; Catarrhini; Hominidae; Homo. the EMHL/GenBank/DDBJ databases. 1; - 1 MW; E64E0794A1B4DB7D CRC64;	ore 83; DB 4; Length 249; dd. No. 1.2e-05; fismatches 0; Indels 0; Gaps 0; fismatches 0; Indels 0; Gaps 0; fismatches 0; Indels 0; ed) sequence update) annotation update)
092619 095712 09411R1 09411B1 09401B1 095033 096033 096033 096033 096033 096033 096033 096033 096035 096035 096035 096035 096035 096035 096035 096035 096035 096035 096035	ALIGNMENT PRT; 249 Created) Last sequenc Last annotat i SALIVARY PR II. Craniata: i: Catarrhini i: E64E0794A	Scc Pre 0; Pre Creat Last Last
$\begin{smallmatrix} 4 & 0 & 1 & 1 & 4 & 4 & 4 & 4 & 4 & 4 & 4 & 4$	17, C; 17, L4, L4, L9, L6, L6, L6, L6, L6, L6, L6, L6, L6, L6	op op
1115 1115 1115 1115 1115 1115 1115 111	PRELIMINARY; (TrEMBLrel. 17, (TrEMBLrel. 19, (TrEMBLrel. 19, (SIMILAR TO BOVII) RELIGANON; RELIGANON; ROUTHERIA; FOND N.A. (JUN-2001) to the 1901; CAC03546.1;	1000 1000 1000 AEKL 1 AEKL 8 AEKL 8 INARY; Lrel. Lrel. Lrel. Lrel. Lrel.
© © © യ യ യ യ യ യ യ യ യ യ യ യ യ യ യ യ യ	AELI FILEM FILEM TILEM N A A A A A A A A A A A A A A A A A A A	arity OKAQEAE OKAQEAE OKAQEAE TEMBLY TEMBLY TYEMBLY TYEMBLY TORY PR
N N 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	PH (1 (1 (1 (1 (1 (1 (1 (1 (1 (1 (1 (1 (1	Similarity 17; Conser AWQLAKQKAQE
44444444444444444444444444444444444444	ULT 1 000 09BQQ0 09BQQ0 09BQQ0 01-JUN-2001 (TrEMBLrel. 17, Cree 01-JUN-2001 (TrEMBLrel. 17, Last 01-DEC-2001 (TrEMBLrel. 19, Last BA49G10.1 (SIMILAR TO BOVINE SABA49G10.1. (SIMILAR TO BOVINE SABAMMAMMALIA: Ettheria; Primates; Camamamalia: Ettheria; Primates; Camamamalia: Ettheria; Primates; Camamamalia: Ettheria; Primates; Camamamalia: Saguence FROM N.A. Tracey A.; Schmitted (JUN-2001) to the EMHIEMBL; All21901; CAC03546.1: - SEQUENCE 249 AA; 27011 MW; F	dat oca l S l S l S l S l S l S l S l S l S l S
1188 1198 1198 1198 1198 1198 1198 1198	RESULT ON SERVICE OF S	Matches Matche
	RESERVED TO BESSENS SON THE SENSE SON THE SE	Do Ouer Match Matc

```
Q9UETS;
                  094BT0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UET5
Q94BT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                       "A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AF432917: AAL28113: 1: -- SEQUENCE 249 AA: 27110 MW: FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Poddwski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cuery match 55.4%; Score 46; DB 16; Length 858; Best Local Similarity 47.1%; Pred. No. 45; Matches 8; Conservative
                                                                                                                                                                                                                                                           Query Match 100.0%; Score 83; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaceae;
                  Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete protecme.
SEQUENCE 858 AA; 96290 MW; A18F52B6CD5805AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondria ", Natuce 36:133-140(1998).
Nature 396:133-140(1998).
INTELFORM IPRO3593; AAA.
INTELFORM IPRO3593; AAA.
INTELFORM IPRO3593; AAA.Subfam.
InterPro; IPRO01697; ATP_GTP_A.
InterPro; IPRO01209; CLP_AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00300; CLPPROTEASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00382; AAA; 1.
PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004176; Clp_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 NTKWQAEKSKLQQAQKL 476
                                                                                                                                                                                                                                                                                                                                                              1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                        1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00004; AAA; 1.
Pfam; PF02861; Clp_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPB PROTEIN (CLPB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A.
                                    NCBI_TaxID=9606;
                                                                                           TISSUE-PAROTID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MADRID E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ZEA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            092EA9
                                                                                                                                                                                                                                                                                                                                                                                                                                     SULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SULT
```

```
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99017974; PubMed-9799604;
Guipponi M., Scott H.S., Chen H., Schebesta A., Rossier C.,
Antonarakis S.E.;
"Two lsoforms of a human intersectin (ITSN) protein are produced by
brain-specific alternative splicing in a stop codon.";
Genomics 53:369-376(1989).
-! SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
EMBL. AF06443; AAC78610.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada K. Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Sakurai T., Salou M., Seki M., Nayuen M., Palm C.J., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Brull Length CDNA of gene F5024_170/AT5920280."; "Full Length CDNA of gene F5024_170/AT5920280."; "Embl. AXK64015.1; "Embl. F2021_18 A.K64015.1; "F2021_18 A.K64015.1; "F
                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.0%; Score 44; DB 10; Length 1043; Best Local Similarity 61.5%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1220 AA; 137701 MW; 7913DE53134660FF CRC64;
                                                                (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last Sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1220 AA
PRT; 1043 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00054; EFh; 2.
SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 5.
PROSITE; PS00018; EF_HAND; UNKNOMN_2.
PROSITE; PS50002; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                           PUTATIVE SUCROSE-PHOSPHATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P29355; ISEM.
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_repeat.
InterPro; IPR001452; SH3.
Pfam: PF00036; efhand; 3.
Pfam: PF00018; SH3.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERSECTIN SHORT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WOLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 WNLAROKKOHEEK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium-binding.
                                                                01-DEC-2001
01-DEC-2001
                                                                                                                                         01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
```

ö

```
0
                                  ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                   Pucharcos C., Fuentes J.J., Casas C., de la Luna S., Alcantara S., Arbones M.L., Soriano E., Estivill X., Pritchard M.; Alu-splice cloning of human intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome.": Eur. J. Hum. Genet. 0:0-0(1999).

EMBL; AF114488: AAP29953.1: --
HSSP; P29355; ISEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Score 44; DB 4; Length 1220;
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.0%; Score 44; DB 4; Length 1220;
69.2%; Pred. No. 1.4e+02;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1220 AA; 137648 MW; B09FDBEF1C06F487 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERSECTIN LONG FORM.
                                                                                                                                                                                                  13. Created)
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERSECTIN SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1721 AA.
                                                                                                                                                                          PRT; 1220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS50002; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR002048; EF-hand.
Interpro: IPR000261; EPS15_repeat.
Interpro; IPR001452; SH3.
      53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00452; SH3DOMAIN.
SMART; SM00054; EFh; 2.
SMART; SM00027; EH; 2.
Query Match
Best Local Similarity 69.2%
....has 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00036; efhand; 3.
Pfam; PF00018; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.0%
Best Local Similarity 69.2%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 QLQKQKSMEAERL 630
                                                                                               618 QLQKQKSMEAERL 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 QLAKQKAQEAEKL 17
                                                                 5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095216
                                                                                                                                                                                            Q9UNK1;
                                                                                                                                                                          Q9UNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
095216
                                                                                                                                              RESULT
Q9UNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                ВÞ
```

```
Gaps
        MEDLINE—99017974; PubMed-9799604;

Guipponi M., Scott H.S., Chen H., Schebesta A., Rossier C.,
Antonarakis S.E.;
"Two isoforms of a human intersectin (ITSN) protein are produced by brain-specific alternative splicing in a stop codon.";
Genomics S.3.59-376(1998).

-i - SIMILARITY: TO OTHER EF HAND CALCIUM BINDING PROTEINS.

EMBL: AF064244; AAC78611.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ducharces C., Puentes J.J., Casas C., de la Luna S., Alcantara S., Arbones M.L., Soriano E., Estivill X., Pritchard M.; Arbones M.L., Soriano E., Estivill X., Pritchard M.; "Alu-splice cloning of human intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome."; EMBL. J. Hum. Genet. 0:0-0[1999].

-: SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. EMBL; AF114487; AAD29952.1; -.. SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. InterPro: IPR0000008: C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 44; DB 4; Length 1721; 69.2%; Pred. No. 2e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1721 AA; 195559 MW; 851A5CFB2BC4EBFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1721 AA.
                                                                                                                                                                                                                                                                                                                                                                                   SWART; SW0054; EFh; 2.
SWART; SW00054; EFh; 2.
SWART; SW00023; PH; 1.
SWART; SW00235; Ph; 1.
SWART; SW00325; RhoGEF; 1.
SWART; SW00326; SH3; 5.
PROSITE; PSS0004; C2_DOMAIN_2; 1.
PROSITE; PSS0003; PH_DOMAIN, 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                      InterPro: IPR000008; C2.
InterPro: IPR002048; EF-hand.
InterPro: IPR000261; BFS15_repeat.
InterPro: IPR000108; New_cyt_fact_2.
InterPro: IPR001849; PH.
                                                                                                                                                                                                                                                                    Pfam: PF00168; C2; 1. Pfam: PF00168; C2; 1. Pfam: PF00169; efhand; 3. Pfam: PF00169; PH: 1. Pfam: PF001618; S43; 5. PRINTS; PR00499; P67PHOX. PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                        InterPro; IPR000219; RhoGEF.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 69.2...
Best Local Similarity 69.2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERSECTIN LONG ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 QLQKQKSMEAERL 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                            HSSP; P29355; 1SEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding.
TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UNK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9UNK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q9UNK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
δ
```

ö

ααααααααααααααααααααααα

```
ESULT 10
```

```
Ouery Match
Best Local Similarity 57.19
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                           MRPL52 OR 1110047B07RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 AWKLROOKLOEERK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AWQLAKOKAQEAEK 16
                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                            NCB1_Tax1D=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METG OR NMA0275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                           Q9D0Y8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .09JWP0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09JWP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09JWP0
                                                           DD410
DD111
DD11
DD111
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20347328: pubMed-10887074; Walsh P.J., Heltz M.J., Campbell.C.E., Cooper G.J., Medina M., Wang Y.S., Goss G.G., Vincek V., Wood C.M., Smith C.P.; "Molecular characterization of a urea transporter in the gill of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Batrachoididae; Opsanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.0%; score 44; DB 4; Length 1721; 69.2%; Pred. No. 2e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1721 AA; 195421 MW; FC4DE644D8BEA2BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         941. EXP. Biol. 203:2357-2364(2000).
EMBL; AF165893; AAD53268.2; -
INTERPRO, IPRODI117; CU-Oxidase
PROSITE; PS00079; MULTICOPER_OXIDASE1; UNKNOWN 1.
SEQUENCE 475 AA; 52838 MW; 700E2B180445198C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.4%; Score 43.5; D 66.7%; Pred. No. 61; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS00018; EF HAND; UNRNOWN_2.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50002; SH3; 5.
InterPro; IPR000261; EPS15_repeat.
InterPro; IPR000108; Neu_cyt_fact_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                    InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR001452; SH3.
                                                                                                                                                  Pfam; PF00168; C2; 1.
Pfam; PF00103; efhand; 3.
Pfam; PF00103; PH: 1.
Pfam; PF001018; SH3: 5.
PRINTS; PR00459; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00239; C2; 1.
SMART; SM00054; EFh; 2.
SMART; SM00027; EFh; 2.
SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 WKLKKOKKQEKADKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WOLAKOKAQE-AEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618 QLQKQKSMEAERL 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=GILL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UREA TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID = 95145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toadfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09PUQ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PUQ5
```

OUPPEBSCOCXZACXACEFIXKKO

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CSDBL/6J; TISSUE-EMBRYO;

Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Konno H., Adachi J., Fukuda S.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,

Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido I., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Sulvaria Y., Storch K.-F.,

Rymshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MPDLINE=2022556; PubMed=1076119;
Parkhill J., Achtum M., James K.D., Brown D., Chillingworth T.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moules S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 43; DB 11; Length 121; 57.1%; Pred. No. 17; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD: MGI:1916086; Mrp152.
SFOHTENCE: 121 AA; 13658 MW; C024F28F8A5B016A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10).
                                                                                               17, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 AA.
                                                        01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequ 01-DUS-2001 (TrEMBLrel. 19, Last anno 1110047807RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
EMBL; AK004194; BAB23216.1; -.
```

```
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SB28
                              (FRAGMENT)
                                                                                                                                                                               Mayer H.;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9GRG0
                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
023362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09GRG0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96020635; PubMed-8577256;
Loessner M.J., Wendlinger G., Scherer S.;
"Heterogeneous endoliyains in Listeria monocytogenes bacteriophages: a new class of enzymes and evidence for conserved holin genes within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20117992; PubMed-10652093;
Loessorn M.J., Inman R.B., Lauer P., Calendar k.;
"Complete nuclectide sequence, molecular analysis and genome structure
of bacteriophage All8 of Listeria monocytogenes: implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                            . Match 51.8%, Score 43; DB 16; Length 685; Local Similarity 63.6%; Pred. No. 1.1e+02; les 7; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 50.6%; Score 42; DB 9; Length 125; Best Local Similarity 46.7%; Pred, No. 25; Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                       moser, rouse, lead.
InterPro; IPR001212; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002547; tRNA_bind.
Pfam; PF01588; tRNA_bind; l.
PRINTS; PR01041; TRNASYNTHMET.
PROSITE; PS00178; AA_TNA_LIGASE_I; l.
Aminoacyl tRNA synthelase; Ligase; Complete protecome.
SEQUENCE 685 AA; 76984 MW; 07F045915ED3BEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2394; CAB35816.1; -.
125 AA; 14707 MW; AF95EFFAE323ADF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q60253 PRELIMINARY; PRT; 350 AA. 060253; Q47436; Q47434; Q47445; Q47456 (1907-1996 (TEMBLEEL. 01, Created) 01-NOV-1996 (TEMBLEEL. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 16:1231-1241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOL Microbiol, 35:324-340(2000).
EMBL, AJ242593; CAB53816.1; -.
          Nature 404:502-506(2000).
EMBL; AL162752; CAB83583.1; -.
HSSP; P00959; 1MEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         siphoviral lysis cassettes."
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SAWQLAKQKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 AAWSKAKEEVKEVEK 57
meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                  468 WELAKOEGODA 478
                                                                                                                                                                                                                                                                                                  4 WQLAKQKAQEA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage A118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=40521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phage evolution.
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9T194;
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9T194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060253
                                                                                                                                                                                                                                                                                                                                                                                                      Q9T194
                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Alveolata: Ciliophora: Oligohymenophorea: Hymenostomatida;
Tetrahymenina: Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cDNA sequences of three tetrins, the structural proteins of the Tetrahymena oral filaments, show that they are novel cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                              MEDLINE-85236066; PubMed-2989404;
Bruns W., Hoppe J., Tsai H., Bruening H.J., Maywald F., Collins J.,
                                                                Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 5K PA GENE ENCODING PENICILLIN ACYLASE, SEGMENT 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2; Length 350;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%; Score 42; DB 5; Length 731; 69.2%; Pred. No. 1.7e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tellany....
proteins.";
Protist 13:171-180(2000).
EMBL; AJ276471; CAC07819.1; -.
FromenCE 731 AA; 87196 MW; A2FC64972BF06BE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 >227 POTENTIAL.
27 >235 POTENTIAL.
290 >350 POTENTIAL.
350 As; 38903 MW; 1D97970699A751DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TETRIN B PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPRU02692, Penicil_amidase.
Pfam, PF01804; Penicil_amidase, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20419140, PubMed-10965956,
Brimmer A., Weber K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 SNMWVICKSKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 41.2 es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetrahymena thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 QIWKEKAAEAEKL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 OLAKOKAOEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=562;
```

0

```
MEDLINE-9812113; PubMed-9461215; Bevan H., Dean C., Bevan M., Banctoft I., Bent E., Love K., Goodman H., Dean C., Bevan M., Banctoft I., Bent E., Love K., Goodman H., Drost L., Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H., Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N., Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P., Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P., Entian K.D., Riegar M., Schaeffer M., Punk B., Mueller-Auer S., Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A., Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B., Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Breva T., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C., Delsen, J.C., Challes J., M., Klosterman S.,
                                                                                                                                                                     Enkaryota; Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
Schueller C., Chalwatzis N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 297337. CAB10287.1; -.
EMBL, AL161540; CAB78550.1; -.
InterPro; IPR001594; Znf-DHHC.
ProDom; PP01529; Zf-DHHC; 1.
ProDom; PP0030341; Znf-DHHC; 1.
Hypothetical protein.
SEQUENCE 736 AA; 80802 MW; 92D443CDFEE20567 CRC64;
                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Lasi sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 80.8 KDA PROTEIN.
736 AA
                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 391:485-488(1998).
PRELIMINARY:
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCB1_TaxID=3702;
```

0; Gaps

50.6%; Score 42; DB 10; Length 736; 53.3%; Pred. No. 1.7e+02; Live 3: Mismatches 4; Indels

Conservative

Query Match Best Local Similarity Matches 8; Conserv

ď

≿

learch completed: August 6, 2002, 17:09:30
fob time: 932 sec

Sequence:

Run on:

Searched:

Database

Result

```
Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5. SIDSI / 999data/holf-geneseqp-embl/AA1981.
5. SIDSI / 999data/holf-geneseqp-embl/AA1981. DAT: *
5. SIDSI / 999data/holf-geneseqp-embl/AA1984. DAT: *
5. SIDSI / 999data/holf-geneseqp-embl/AA1984. DAT: *
6. SIDSI / 999data/holf-geneseqp-embl/AA1986. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1986. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1986. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1989. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1989. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1991. DAT: *
7. SIDSI / 999data/holf-geneseqp-embl/AA1999. DAT: *
7. SIDSI / 999data/holf-geneseqp-geneseqp-embl/AA1999. DAT: *
7. SIDSI / 999data/holf-geneseqp-geneseqp-embl/AA1999. DAT: *
7. SIDSI / 999data/holf-geneseqp-geneseqp-embl/AA1999. DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haema
Human gene 5 encod
Human gene 5 encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parotid secr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parotid secr
PRO1025 prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3D1A prote
                                                                                                                                                                   (without alignments)
13.629 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
                                                                                                                                               August 6, 2002, 16:52:52; Search time 138.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Нишап
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Нишап
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                              747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                       US-10-020-139-2_COPY_68_84
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69221
AAW60682
AAB24069
AAB25765
AAB75351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE04221
AAB94691
AAY32158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM90448
AAE04203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM25745
                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                           1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
123
123
595
641
                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883
883
883
844
846
846
847
                                                                                                                                                                                                                                                                                                                                          Scoring table:
```

	12	5	ω.				Ниша	[od u
	13	4	m				Human	SH3D1A pro
	14	φ. Ωι	٠ :	,			Nove	1 հս աձ ո d
	15	4 4 U ft	η. Υ	٦.			Huma	polypeptide
	17	. 4	. n				Human	SH3DIA
	18	4.0	ش د	_			Humai	n SH3D1A prote
	20	42 5	9.0	557	19	AAY50199 AAW57840	Stre Wild	Streptococcus pyog Wild type penicill
	21	2.0	5				V56T	mutant penici
	23	2 C	-				F24A	mutant penici
	24	10					F24L	mutant penici
	25	2 2 2	6				Sedne	nce encoded b
	26	20					A.	aecalis-E. col
	28						Dros	ophila meianog
	29	1 4					Pol v	n process seguen
	30	1 4	6	-			Ente	rococcus faeca
	31	H C	თ. ი				Pseu	domonas aerugi
	2 K	00	 				Ardb	idopsis thalia
	34	0 4	œ.				Arab	idopsis thalia
	35	4.	m				Arab	idopsis thalia
	35	20	ກໍດ				Dros	ophila melanog
	. 80	4 4					a s	opulla meranog
	36	. 4	 m				Dros	ophila melanog
	0,	40 4	m				Neis	seria gonorrhe
	, n	ν. 4.					Tryp	anosoma cruzi
	ייי ני	υ. rc. 4. 44					xepe Sen+	sequence
	44 39	. 4	. ~			AAW26536	Tryp	oma cru
	e E	5.					rp,	oma cruzi
						ALIGNMENTS		
RES	JLT							
7	69221 AAW6922	l sta	ndard	Δ,	rotein;	249 AA.		
×	5							
₹×	AAWO 922							
LQ?	16-OCT-	1998	(fi	rst entry)	ry)			
DE	Human p	arotid	secr	cretory	prot	ein.		
× 3 3 3	Parotid non-imm	id secretor	tens	prote ive di	in; sord	SP; digestive ; immune syste	disorder; endocrin m disorder; cancer	ine disorder; er; human;
×	1)					
SOX	ното за	piens.						
FF	Key Peptide	ā		Locatio 118	n/Qne	lifiers		
FT FT	Protein			/note= "signal 19249 /note= "mature	"sigr "matu	al peptide" re hPSP"		
X d	WO98284	20-A1.						
XX CP	02-JUL-	1998.						
X Y	18-DEC-	1997;	σ,	7WO-US2352	3522.			
X a	73-080-	1996	ā	, e 00 - 5118	d			
XX	2	4	n	_	7			
PA	(HUMA-)	HUMAN	GE	GENOME SCI	IINC			

```
WO9821329-A1.
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-1996;
                                                                                                                                                                                                                       18-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1998.
Sednence
                                                                                                                                                                                               AAW60682;
                                  Query Match
                                                                                                                                                          4W60682
```

```
Claim 1; Fig 1A-C; 65pp; English.
  gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200053755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24069
      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific acids, which are potentially useful for treating conditions associated with are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affnity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secretory tissue; gastrointestinal tissue; HPSP. Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pandrealitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New parotid secretory protein - useful for, e.g. treatment of cancer
                                                       New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parotid secretory protein; human; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 83; DB 19; Length 249; 100.0%; Pred. No. 5.9e-05; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and auto-immune disease, particularly of secretory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW60682 standard; Protein; 249 AA.
                                                                                                                                    Claim 16; Fig 1; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US20651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-074928B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ssawglakgkaqeaekl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WFI; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 AA;
                N-PSDB; AAV44759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV37699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandman O,
```

```
This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, castrointestinal tissue, e.g. cancer of salivary gland, thyroid, crows disease, thyroiditis, insulin-dependent diabetes, pancreatis, of saves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastrifis, Host ceils to containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; etcomal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation; tumourigenesis; identification; can er; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 83; DB 19; Length 249
100.0%; Pred: No. 5.9e-05;
^ Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1025 protein sequence SEQ 1D NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB24069 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US12252.
99US-0141037.
99US-0143048.
99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US28313.
99WO-US30911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 ssawqlakqkaqeaekl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
```

```
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial stronal and blastocoelic disorders, and inflammatory, andiogenic and immunologic disorders. AAC58242 to AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58367 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                           one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO830, PRO848, PRO643, PRO105, PRO1005, PRO1009, PRO1015, PRO1017, PRO1017, PRO10111, PRO1153, PRO1030, PRO1031, PRO1051, PRO1187, PRO1281, PRO23, PRO39, PRO34, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRÔ polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Caps
                                                                       Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer \cdot
                                                                                                                                               that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 83; DB 21; Length 249; 100.0%; Pred. No. 5.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                 The present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein SEQ ID #77.
                                                                                                                    Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0113686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.º
Best Local Similarity 100.º
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 ssawqlakgkaqeaekl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    septic shock; impotence.
 Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention.
                              WPI; 2000-572270/53.
                                              N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200037491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB25765
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

```
This sequence represents a human secreted protein amino acid sequence.
The invention relates to sequences AAA87725 x88774 which encode human
secreted proteins AAB2703-B25812. The proteins include signal peptides.
Included in the invention are a host cell containing one of the CDNA sequences, and a purified antibody capable of binding to one of the CDNA sequences to binding to one of the Storing the sequence data on a computer system, and a method for accreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for admitivying features of the CDNA sequences using a computer programme.
The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins and any and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention expression vectors and secretion vectors. The proteins of the invention disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, and impotence.

C dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                    Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 83; DB 21; Length 249; 100.0%; Pred. No. 5.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                     Bouqueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0141032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0469099.
   99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ssawglakgkageaekl 84
                                                                                                                                                                                                                                                                                                                                                                             mapping procedures -
                                                                                                                                                                                                      WPI: 2000-442637/38.
                                                                                                                                                                                                                                           N-PSDB; AAA87727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET.
                                                                    (GEST ) GENSET.
25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB75351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
```

·;

```
Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WU200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - FEB - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM90448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM90448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiinbacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fundicide; antimutagen; cardiovascular; antianaemic; anemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatopological; antiallergic; antiathamatic; antidatheut; contrological; antidiperessant; nocropic; antiparkinsonian; informanciumunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                     49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
                                                                                                                                                            The present invention relates to 49 Secreted proteins and the CDNAS encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antianaphylactic, rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                             100.0%; Score 83; DB 22; Length 249; 100.0%; Pred, No. 5.9e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Indels
Jobert S;
Dumas Milne Edwards J, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM25745 standard; Protein; 260 AA.
                                                                                                                            Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                          68 ssawqlakqkaqeaekl 84
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEL; 2001-457603/49.
                                   WPI; 2001-071487/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-FSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM25745;
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3SULT
4M25745
```

```
encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation. Theumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immundeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple solerosis, depression, Alzheimer's disease, parkinson's disease, neurodegenerative and
AAM25953. The proteins can have activities based on the tissues and realist they are expressed in, such as; antinflammatory, antirheumatic; antiatthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiaut; cardiavascular; antianaemic; antiagregant; haemostatic; vulnerary; antidates; costeopathic; dermatological; antiallergic; antiantigic antidiabetic; vulnerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiquality indication antidiabetic; or antidial individual antiquality individual individual antiquality individual indivi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen SEQ 1D NO:18041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 83; DB 22; 100.0%; Pred. No. 6.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; gene therapy; vaccine; metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM90448 standard; Protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0179065.
2000US-0180628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0216647.
2000US-0216880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0186350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0190076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0214886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0189874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0205515
2000US-0209467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0198123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0217496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 ssawqlakqkaqeaekl 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurological disorders.
```

0001S-022996 0001S-022996 0001S-022996 0001S-022951 0001S-022952 0001S-022526 0001S-022526 0001S-022526 0001S-022526 0001S-022526 0001S-022526 0001S-022526	1000US - 0225888. 1000US - 0227868. 1000US - 022947. 1000US - 02314.
700-20 700-20	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	72 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

```
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 18041; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM;
20000S-0246474.
2000US-02464775.
2000US-02464776.
2000US-0246478.
2000US-0246523.
2000US-0246524.
2000US-0246526.
2000US-0246527.
2000US-0246527.
2000US-0246527.
2000US-0246619.
2000US-0246619.
                                                                                                                                         2000US - 0246613
2000US - 0249207
2000US - 0249209
2000US - 0249210
2000US - 0249210
2000US - 0249210
2000US - 0249213
2000US - 0249213
2000US - 0249214
2000US - 0249214
2000US - 0249216
2000US - 0249245
2000US - 0249265
2000US - 0249265
                                                                                                                                                                                                                                                                                                                     2000US-0249300,
2000US-0250160,
2000US-0250391,
                                                                                                                                                                                                                                                                                                                                                         2000US-0251988.
2000US-0256719.
2000US-0251479.
                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0251869.
2000US-0251989.
2000US-0251990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME, SCI INC
                                                                                                                                                                                                                                                                                                                                                  2000US-0251030
                                                                                                                                                                                                                                                                                                                                                                                     20000S-0251856.
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0251868.
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-2000; 2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483426/52.
N-PSDB; AAK63229.
                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
                                                                                                                                                                    17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                          17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                     17 - NOV - 2000;
17 - NOV - 2000;
17 - NOV - 2000;
                                              08-NOV-2000;
08-NOV-2000;
                                                                 08-NOV-2000;
                                                                          08-NOV-2000;
                                                                                            08-NOV-2000;
                                                                                                     08-NOV-2000;
                                                                                                                       08-NOV-2000;
                                                                                                                                08-NOV-2000;
                                                                                                                                                  17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                NOV-2000;
                                                                                                                                                                                                        NOV-2000;
                                                                                                                                                                                                                   17-NOV-2000;
                                                                                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                    17-NOV-2000;
```

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and and a sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome expression by rectifying mutations or deletions in a patient's genome supplement the patients on production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the

```
protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87594 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheunatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; asthma; skin disorder; psordase; cognitive disorder; schizophrenia; asthma; skin disorder; psordasis; sepeis; diaberes; etheroselerosis; cardiovasqular disorder; pregnancy-related disorder; gene therapy; enforcer; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 5 encoded secreted protein HUVFB80, SEQ 1D NO:57.
                                                                                                                                                                      Score 46; DB 22; Length 85; Pred. No. 8.1;
                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Komatsoulis GA, Baker KP, Young PE;
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 436-437; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              AAE04203 standard; Protein; 123 AA
                                                                                                                                                                                                      3;
                                                                                                                                                                        55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2000; 2000WO-US31162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0166415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000US-0215136.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                          3 AWQLAKQKAQEAEK 16
                                                                                                                                                                                                                                                                          52 awglrggklgeegr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-343793/36.
                                                                                                                                                                                     Local Similarity
Les 8; Conserva
                                                                                                                       85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD08492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200136432-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001
                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                               AAE04203;
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             AE04203
                                                                                                                                                                                                                                                                                                                               ESULT
   OOOOOOXQ
                                                                                                                                                                                                                                                                           ō
```

```
The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be disposed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the disposis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease, conquitive disorders, schizophenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, skindney disorders, cardiovascular disorders, anglogenic disorders, skindney disorders.
                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorders, pregnancy related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene 5 encoded secreted protein HUVFB80, SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.4%; Score 46; DB 22; Length 123; 57.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by GKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE04221 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 awglrggklgeegr 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AWQLAKQKAQEAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200136432-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE04221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE04221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

```
RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY32158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
   δ
                                                                                                                                                                                                                                                                                                        AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the and include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of abnormalities, haematopoietic disorders, diseases of the immune system, and include developing products for the diagnosis or treatment of abnormalities, neurological disorders, disorders, diabetes, atherosclerosis, allergies, neurological disorders (e.g., Alzheimer's disease, partnam, alsorders, endocrine alsorders, and infections. The proteins can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound sastrointestinal disorders, prequency related disorders, endocrine can animal organs before transplantation, for supporting coll collure of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used in as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in allerating symptoms associated with the disorders mentioned above, and in diagnostic immunososays or enzyme linked immunososays or enzyme linked invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%; Score 46; DB 22; Length 123; 57.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                       Ruben SM, Komatsoulis GA, Baker KP, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 12;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:15659.
                                                                                                                                                                                                                                                                               Claim 11; Page 453; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB94691 standard; Protein; 595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                           19-NOV-1999; 99US-0166415.
30-JUN-2000; 2000US-0215136.
                                           15-NOV-2000; 2000WO-US31162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 57.1
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 awglrggklgeegr 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AWQLAKQKAQEAEK 16
                                                                                                                                                                                    WPI; 2001-343793/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 123 AA;
                                                                                                                                                                                                     N-PSDB; AAD08511
   25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB94691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
δ
```

```
polynucleotide which comprises a 3' end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5' end sequence/3' end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polyucisetide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides: or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 -end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH1362 represent human cDNA sequences; AAB92446 to AAH3639 represent human amino acid sequences; and AAH3639 to AAH33632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.0%; Score 44; DB 22; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 15659; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32158 standard; Protein; 641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa T,
                                                                                                                                                                                                                                                                                                                               27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                               99.JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELLI -) HELLIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 qlqkqksmeaerl 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human SH3D1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3est_Local Similarity
4atches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
Homo sapiens.
                                                                       EP1074617-A2.
                                                                                                                                                                                                                                                                                               29-JUL-1999;
                                                                                                                                                 07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32158;
```

ö

```
..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the protein encoded by the human SH3DIA CDNA clone 9 (see AA24574). SH3DIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The cromosome 21. The protein includes SH3 domains and EH4 domains, both associated with protein-protein interactions and the latter chromosome 21. The protein-protein interactions and the latter with maintenance of the cytoskeleton. At least 3 isoforms of SH3DIA exist (see AA712154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, related alsorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of chromosome 21, low platelets in deletion for 21, association of disorders including brain malformalities, dysfunctions and disorders including brain malformations and disorders and object half when the also provided: for suppressing and colpocephaly, methods are also provided: for suppressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and
                 SH3D1A; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; patalet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells unable to regulate themselves; screening for a somaticalteration in the SH3D1A gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             megakaryoctyjc abnormality, myeloproliferative disorder,
haematopoietic disorder, platelet disorder or leukaemia; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.0%; Score 44; DB 20; Length 641; Best Local Similarity 69.2%; Pred. No. 1.3e+02; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening of drugs for cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                         (CEDA-) CEDARS SINAI HEALTH SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARM93229 standard; Protein; 642 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Fig 15; 99pp; English.
                                                                                                                                                                                                                                                                                              99WO-US08371.
                                                                                                                                                                                                                                                                                                                                            98US-0082007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 glgkgksmeaerl 127
                                                                                                                                                                                                                                                                                                                                                                                                                                  Korenberg JR, Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 5 QLAKOKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-633829/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ34574.
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                      W09953062-A2.
                                                                                                                                                                                                                                                                                              16-APR-1999;
                                                                                                                                                                                                                                                                                                                                            16-APR-1998;
                                                                                                                                                                                                                                                    21-0CT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM93229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AM93229
<u>≻</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

```
The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been solated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA asily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3D1A; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                       Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 2647; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.0%; Score 44; DB 22; Length 642; 69.2%; Pred. No. 1.3e+02; tive 2; Mismatches 2; Indels
                                                         Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32157 standard; Protein; 648 AA.
             Human polypeptide, SEQ ID NO: 2647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use in genetic manipulation -
                                                                                                                                                                                                                                                                                  2000JP-0118774.
                                                                                                                                                                                                                       07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 glgkgksmeaerl 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human SH3DlA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAK94139
                                                                                                                                                                                                                                                              08-JUL-1999;
                                                                                                  Homo sapiens.
                                                                                                                                        EP1130094-A2
                                                                                                                                                                                                                                                                                       11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                 05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32157
```

```
Caps
                                                                                                                                                                                                                                                                                      Nucleic acid from the human SH301A gene and its products, useful for
the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the protein encoded by the human SH3DIA cDNA clone 5 (see AA234573). SH3DIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene maps to the small candidate region for low platelets on chromosome 21. The protein includes SH3 domains and EH domains, both associated with protein includes SH3 domains and EH domains. SH3D1A exist (see AAY32154-58). The invention provides methods for myeloproliferative disorder, platelet disorder, acute leukaemia, meloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder acute leukaemia, chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lissencephaly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methods are also provided: for suppressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells unable to regulate themselves; screening for a somation alteration in the SH301A gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyjc abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.0%; Score 44; DB 20; Length 648; 69.2%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening of drugs for cancer therapy.
                                                                                                                                                      (CEDA-) CEDARS SINAI HEALTH SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Fig 13; 99pp; English.
                                                                            99WO-US08371.
                                                                                                                 98US-0082007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618 glgkgksmeaerl 630
                                                                                                                                                                                           Chen X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                 WP1; 1999-633829/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and colpocephaly.
                                                                                                                                                                                                                                                   N-PSDB; AA234573.
                                                                                                                                                                                              Korenberg JR,
W09953062-A2.
                                                                          16-APR-1999;
                                                                                                                 16-APR-1998;
                                     21-0CT-1999
                                                                                                                                                                                                                                                                                                                              leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
  ⋩
```

```
Best Loca
Matches
                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #20566.
                                                                                                                                                                                                                                                                                                    ABG20575 standard; Protein; 932 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   ABG20575;
```

9

W0200175067-A2.

Homo sapiens.

```
polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The useful for chromosome polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. AGG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.0%; Score 44; DB 22; Length 932; 69.2%; Pred. No. 1.9e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ 1D No 50934; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM43519 standard; Protein; 1035 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 197.
                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                        31-MAR-2000; 2000US-0540217.
                                                                                                                                                      23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 69.2 les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 glgkgksmeaerl 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 AA:
                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS84762
                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity
                     11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM43519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

ö

us-10-020-139-2_copy_68_84.rag

Page 10

```
×
                                                                                                                              31-JAN-2000; 2000US-0179065.

24-FEB-2000; 2000US-018062B.

25-FEB-2000; 2000US-018062B.

16-MAR-2000; 2000US-018074.

17-MAR-2000; 2000US-019076.

18-APR-2000; 2000US-0190125.

19-APR-2000; 2000US-0190125.

28-JUN-2000; 2000US-015135.

07-JUL-2000; 2000US-0151486.

11-JUL-2000; 2000US-0151486.

11-JUL-2000; 2000US-022525.

11-JUL-2000; 2000US-022526.

11-JUL-2000; 2000US-022526.

11-JUL-2000; 2000US-022526.

11-JUL-2000; 2000US-022526.

11-JUL-2000; 2000US-022526.

11-AUG-2000; 2000US-02293.

11-AUG-2000; 2000US-02293.

11-AUG-2000; 2000US-02323.

11-AUG-2
                                                                                                      17-JAN-2001; 2001WO-US01309
                                          W0200155308-A2.
              Homo sapiens.
                                                                      02-AUG-2001.
```

000US - 023548 000US - 023583 000US - 023635 000US - 023636 000US - 022636 000US - 022636 000US - 022637 000US - 022637 000US - 023703 000US - 023993	0000S - 024178 0000US - 024178 000US - 024180 000US - 024180 000US - 0246180 000US - 024617 000US - 024647 000US - 024647 000US - 02467 000US - 024652 000US - 024652	
6-SEP-200 7-SEP-200 9-SEP-200	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	

```
(AUMA-) HUMAN GENOME SCI INC.
```

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488781/53.

N-PSDB; AAI63825

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -

Claim 11; SEQ ID NO 197; 664pp + Sequence Listing; English.

The invention relates to human polynucleotides (AA163803-AA164012) and the invention relates to human polynucleotides (AA16303-AA164012) and the encoded proteins (AAM34497-AAM3660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists or are useful in the diagnosis, treatment and prevention of: (a) cancer, c.g. beest and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uroganital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, c.c. croin's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colliss, (c) ardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Con the parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.

Con the parasitic infections was obtained in electronic format directly from MIPO at ftp.WiPo.int/Published_pct_sequences.

Sequence 1035 AA;

.. O 0; Gaps Ouery Match 53.0%; Score 44; DB 22; Length 1035; Best Local Similarity 69.2%; Pred. No. 2.2e+02; Matches 9; Conservative 2; Mismatches 2; Indels (

5 QLAKQKAQEAEKL 17 $\stackrel{\sim}{\sim}$ 629 glqkqksmeaerl 641

Search completed: August 6, 2002, 16:52:53 Job time: 335 sec

```
90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                      US-08-793-229-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-793-229-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12, Appl
12, Appl
5268270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Appl
Sequence 143, App
                                                                                        (without alignments)
8.107 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 34, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43,
Sequence 43,
Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12,
                                                                          August 6, 2002, 16:53:54; Search time 51.22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2
Sequence 2
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/jaa/5A_COMB.pcp:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pcp:*
/cgn2_6/ptodata/2/jaa/AA_COMB.pcp:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pcp:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pcp:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pcp:*
           Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-541-780-6
US-07-7311-157A-5
US-08-541-780-6
US-08-557-309B-27
US-08-993-674A-27
US-08-993-674A-43
US-08-993-674A-43
US-08-993-674A-43
US-08-185-160-13
US-08-185-160-13
US-08-185-160-11
US-08-185-160-11
US-08-185-160-11
US-08-185-160-11
US-08-185-160-11
US-08-185-160-13
US-08-144-1015-13
                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-997-080-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-793-229-33
US-09-285-957-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-731-157A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-843-530B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-793-229-34
GenCore version 4.5
                                                                                                                                                                                                                       231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                   US-10-020-139-2_COPY_68_84
83
                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                      1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                     [ssued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
                                                                                                                                                                                                                                                                          disimum DB seq length: 0 daximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Score Match Length DB
                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fitle:
Perfect score:
                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sedneuce:
                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (esult
```

```
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                             Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                  Sequence sequence sequence
  Sednence
                                                                                                                           Seguence
                                                                                                                                      Sequence
                                                                                                                                                                                                                Sequence
                          Sequence
                                                   Sequence
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                    Sequence
                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                  US-08-356-354-6
US-08-78-656-6
US-08-778-656-4
US-08-778-656-4
US-08-905-223-395
US-08-905-223-395
US-08-964-127-4
                                                                       US-09-355-166-9
US-08-553-436A-6
US-09-336-447A-76
                                   US-08-961-083-102
US-09-095-855-196
                                                             US-08-408-095-21
                                                                                                                         PCT-US95-08565-7
                                                                                                             US-08-272-255-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 64;
5; Mismatches
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%; Score 42;
41.2%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/EP95/03249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/793, 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/08793229
Patent No. 5891703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 41.2 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSAWQLAKQKAQEAEKL 17
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                         Patent No. 5891703
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
```

1 SNMWVIGKNKAQDAKAI 17

```
50.6%; Score 42; DB 3; Length 555; 41.2%; Pred. No. 64; 5; Indels ntive 5; Mismatches 5; Indels
                                                                                             APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: OUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: POCTOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/285,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VAN DER LAAN, Jan Metske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/09285957
Patent No. 6033823
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/793,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08793229 Patent No. 5891703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 97C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNMWVIGKNKAQDAKAI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicago
                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                         90909
                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ī
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
ESULT 2
S-09-285-957-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-09-285-957-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 3
5-08-793-229-33
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 42; DB 2; Length 557; 41.2%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INSTITUTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.6%; Score 42; DB: Best Local Similarity 41.2%; Pred. No. 64; Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                              APPLICATION NUMBER: PCT/EP95/03249
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            97075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/09285957
Patent No. 6033823
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/793,229
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 970
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312)913-0001
TELEFRAX: (312)913-0002
INFORMATION FOR SEQ 1D 002
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNMWVIGKSKAQDAKAI 17
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                               FILING DATE: 23-APR-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-793-229-33
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-285-957-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
```

290 SNMWVIGKNKAQDAKAI 306

g

```
Query Match

S0.6%; Score 42; DB 3; Length 557;
Best Local Similarity 41.2%; Pred. No. 64;
Matches 7; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 42; DB 1; Length 844;
41.2%; Pred. No. 98;
tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) COMENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COOLEY GODWARD CASTRO HUDDLESON & TATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : FIVE PALO ALTO SQUARE, 4TH FLOOR
PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAE-VENTER PH.D., BARBARA
RATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07731157A
Patent No. 5457032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: ATCC 21285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 844 amino acids
AMINO ACID
                                                                                                                                                                                                                             1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                1 SNMWVIGKSKAQDAKAI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 41.28
Matches 7; Conservative
TYPE: amino acid
STRANDEDNESS: single
                     : STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-957-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                 US-07-731-157A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                  q
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 42; DB 2; Length 844; 41.2%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: LHW PC COMPALIALE
COMPATION: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                             APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Wisset, Onno
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta lactam acylase genes
CORRESPONDENCE: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GBRO-027/00US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: RAE-VENTER PH.D., BARBARA REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP 90200962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Sequence 5, Application US/07731157A ; Patent No. 5457032
                                  . Sequence 6, Application US/08541780 ; Patent No. 5935831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OKGANISM: Kluyvera citrophila
STRAIN: ATCC 21285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quax, Wilhelmus J.
Misset, Onno
Van der Laan, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: '6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               844 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 SNMWVIGKNKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 41.29
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-731-157A-5
RESULT 6
US-08-541-780-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-541-780-6
                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

ö

5; Indels

1 SSAWQLAKQKAQEAEKL 17

Σ.

```
50.6%; Score 42; DB 1; Length 846; 41.2%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; indels
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Milhelmus J.
APPLICANT: Wan der Laan, Jan M.
APPLICANT: Van der Laan, Jan M.
TITLE OP INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Haug, H
AUTHORS: Buckel, P
AUTHORS: Bock, A
TITLE: Penicillin acylase from E.coli: unique
TITLE: gene-protein realtion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/COCKET NUMBER: GRO-027/00US
TELECOMMUNICATION INFORMATION:
TELECAX: 415-494-7622
TELECAX: 415-857-0663
TELECAX: 380816 COOLEY PA
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 98;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
FILLIG DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08541780 Patent No. 5935831 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schumacher, G
Sizmann, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 SNMWVIGKSKAQDAKAI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 41.28
watches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME: 14
PAGES: 5713-5727
NATE: 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                        94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-07-731-157A-5
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 8
S-08-541-780-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
```

```
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION ON NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 42; DB 2; Length 846;
41.2%; Pred. No. 98;
tive 5; Mismatches 5; Indels
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
              E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUANE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Bock, A TITLE: Penicillin acylase from E.coli: unique TITLE: gene-protein realtion. JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                               PEREFERENCE/DOCKET NUMBER: 32,750

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: GBRO-027/00US
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PAPLICATION NUMBER: EP 90200962
FILING DATE: 18 APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/08557309B ; Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 846 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schumacher, G
Sizmann, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSAWQLAKQKAQEAEKL 17
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
CORRESPONDENCE ADDRESS:
                                                       PALO ALTO CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Наид, Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 5713-5727
DATE: 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: line
MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                  94306
                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-557-309B-27
                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-541-780-5
                                                                          STATE:
```

```
PREVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Schil, John M.
APPLICANT: MICHAELL, Patricia D.
APPLICANT: MICHAELL D.
APPLICANT: LOT MICHAELL D.
APPLICANT: LOT MICHAELL D.
APPLICANT: LOT MICHAELL D.
APPLICANT: MICHAELL D.
APPLICANT: MICHAELL D.
APPLICANT: MICHAEL D.
APPLICANT: MICHAELL D.
APPLICANT: MICH
                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                  47.6%; Score 39.5; DB 3; Length 40; 60.0%; Pred. No. 10; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.6%; Score 39.5; DB 4; Length 40; 60.0%; Pred. No. 10; Live 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210121.422C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/993,674A
18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Sequence 27, Application US/08993674A . Patent No. 6228372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 21
      TELEFAX: (206) 682-6031
INFORMATION FOR SEQ 1D NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 622-49(
(206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed, Steven G.
                                                                                                     40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 60.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 AWQEAEERAQREAEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AWQLAKOKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AWQEAEERAQREAEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seattle
Washington
                                                                                                                               amino acid
                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-993-674A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-993-674A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                       US-08-834-306-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.6%; Score 39.5; DB 2; Length 40; 60.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
CERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/557,309B FILING DATE: 14-NOV-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MAKI, David J. REGISTATION NUMBER: 31,392 REPERENCE/DOCKET NUMBER: 210121.422 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210121.422C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08834306
Patent No. 6054135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ 1D NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 40 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 AWQEAEERAQREAEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-557-309B-27
                                                                                                                                                      98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                      STREET: book C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 CONTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-834-306-27
                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

ò ρp

```
PREVENTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Scalif, John M.
APPLICANT: MCNAFIL, Patricia D.
ATTLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEC ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                47.6%; Score 39.5;
      CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/834,306
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08993674A; Patent No. 6228372
CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.08;
                                                                                                                                                                                                                                                                                      LENGTH: 186 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 186 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AWQEAEERAQREAEE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Than 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-993-674A-43
                                                                                                                                                                                                                                                                                                                                                                   US-08-834-306-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                      PREVENTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREVENTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                               APPLICANT: Reed.Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                    E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JE: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.6%; Score 39.5; [60.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210121.422
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
                        Sequence 43, Application US/08557309B Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/08834306 Patent No. 6054135 CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| |:::|| |||:
|||| AWQEAEERAQREAEE ||| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                 Patent No. 5916572
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
S-08-557-309B-43
        IS-08-557-309B-43
                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-08-834-306-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
```

```
1; Gaps
                                                     47.6%; Score 39.5; DB 4; Length 186; 60.0%; Pred. No. 50; tive 4; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                     Sequence 13. Application US/09185160
Patent No. 6252137
APPLICANT: ODELL, JOAN T.
APPLICANT: ARADER, PATRICIA A.
APPLICANT: HARDER, PATRICIA A.
TITLE OF INVENTION: SOVBEAN HOWOLOG OF A SEED-SPECIFIC TITLE OF INVENTION: UNLARIS
TITLE OF INVENTION: UNLARIS
TITLE OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.4%; Score 38.5; DB 4; Length 734; 52.9%; Pred. No. 2.9e+02; tive 3; Mismatches 4; Indels 1
                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/185,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,459
FILING DATE: NOVEMBER 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 302-773-0164
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 734 amino acids
TYPE: amino acid
STRANDEDNESS:
                                 Ouery Match
Best Local Similarity 60.00
For 9, Conservative
                                                                                                                                                    Query Match
Best Local Similarity 52.9 Matches 9; Conservative
                                                                                                                          3 AWQLAKQKAQ-EAEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : TOPOLOGY: linear
: MOLECULE TYPE: peptide
JS-09-185-160-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
US-08-993-674A-43
                                                                                                                                                                                                                      RESULT 15
US-09-185-160-13
                                                                                                                                                              q
                                                                                                                            οy
```

4; Indels 1; Gaps

1 SSAWQLAKQKAQE-AEK 16

λ

iearch completed: August 6, 2002, 16:53:55
 ob time: 287 sec

Carried Company Committee

```
H-transporting AT
probable ABC trans
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      topolsomerase IV s
topolsomerase IV c
topolsomerase IV s
DNA topolsomerase
DNA topolsomerase
DNA topolsomerase
                                                                                                                                                                                                           August 6, 2002, 17:05:15 ; Search time 66.51 Seconds (without alignments) 13.003 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical prote hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     topoisomerase IV c
topoisomerase IV c
DNA-directed RNA p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acid/phospho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carboxyl-terminal
NADP-dependent mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-alanine aminotra
GDP dissociation i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical prote
farnesyltranstrans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              topoisomerase IV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283138 segs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                      US-10-020-139-2_COPY_115_123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ost-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T21644
T10290
AB2118
C87689
A83218
S30597
C83339
D69989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF3134
F98153
T16268
G82078
B83026
T43812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S33711
F91118
E85963
AE0889
AG0082
T28156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI0641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D65090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        finimum DB seq length: 0 taximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \begin{array}{c} \mathbf{u} \\ \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atabase :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             searched:
                                                                                                                                                                                                                              dun on:
                                                                                                                                                                                                                                                                                                                                                                                  ltle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             esult
```

	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		44444444444444444444444444444444444444	ииииииииииии	137082 856024 856024 856024 8364091 108293 108293 108293 108293 108293 108293 119203 11930203	GDP-dissociation is Smg p25A regulator GDP dissociation is Tab GDP dissociation in VUPBH12R.39. homol hypothetical protein R10D2.6 (imitogen-activated Chemotaxis protein can tip fiber pro
-			1139 3263 134	000	NMENTS	hypothetical prote hypothetical prote hypothetical prote
RESULT AIO641 FAICK 1 C;SPEC C;Dec C;Dete	LT 1 41 y acid/phos ecies: Saln te: this sp te: 09-Nov-	spholipic monella e pecies ha -2001 #se	d synth enteric as also equence	esi: a si: i bee	cein Plsx [in enterica sei lled Salmonel	Salmonella enterica subs nge 27-Nov-2001
R;Pa th, 'S', 'S', 'S', 'S', 'S', 'S', 'S', 'S	rkhill, J.; I.; Connert; Moule, S.	Dougan, Lon, P.; O'Gaoi	Gronin Cronin	ame,	; K.D.; Thomson, N.R.; Pickard, ; Davis, P.; Davies, R.M.; Dowd	ard, D.; Wain, J.; Churc Dowd, L.; White, N.; Far
A, Au A, Til A, Rei A, Rei A, Ste	thors: Pari tle: Comple ference num cession: Al	ry, C.; Cete genominger: AB(10641	Duail, Duail, D502; P	M	erford, K.; Simmonds, n multiple drug resist 1608	M.; Skelton, J.; Stevens, ant Salmonella enterica s
A); Red C); Ger C); Ger C); Sur C); Sur	A.Residues: 1-359 <par> A.Cross-references: GB:AL513382; PIDN:C:Genetics: A:Gene: STY1231 A:Gene: STY1231 C:Superfamily: phospholipid synthesis</par>	SS9 <parsices: gb:<="" td=""><td>AL5133</td><td>82; ynt}</td><td>382; PIDN:CAD08316.1; PID:g16502362 Synthesis protein</td><td>862; GSPDB:GN00176</td></parsices:>	AL5133	82; ynt}	382; PIDN:CAD08316.1; PID:g16502362 Synthesis protein	862; GSPDB:GN00176
Que Bes Mats Qy Db	Query Match Best Local Sin Matches 7; 1 EPIDDA 345 EPLDDO	tch al Similarity 7; Conserva EPIDDGKGL 9 : : EPLDDGKGV 353	8 7 vati	7 . 8 %; v.e. v.e.	Score 44; DB 2; Length 35 Pred. No. 0.99; 2; Mismatches 0; Indels	59; 5 0; Gaps 0;
RESULT T21644 hypothe C,5peci C,5peci C,Acces R,Basha submitt	SULT 2 Tothetical protein F32B6.9 - Car Species: Caenorhabditis elegans Date: 15-Oct-1999 #Sequence_rev: Accession: T21644 Basham, V. Dmitted to the EMBL Data Library Reference number: 219453	otein F3 Orbabdit 1999 #se 1644 e EMBL D	12B6.9 is electronerical controls (12 Penal controls) (12 Penal co	9 - Caend legans ce_revis Library,	- Caenorhabditis elegans gans _revision 15-Oct-1999 #text_change brary, October 1996	ge 15-oct-1999
A, Shoo A, Shoo A, Res A, Exp A, Exp A, Gen A, Map	A; Accession: T21644 A; Status: preliminary; translated fi A; Status: preliminary; translated fi A; Molecule type: DNA A; Residues: 1-413 <wil> A; Cross-references: EMBL: 281074; PII A; Experimental source: clone F3286 C; Genetics: A; Gene: CESP: F3286.9 A; Map position: 22/2. 6177: 747.2.176.2.</wil>	1644 minary; : DNA 13 <wil> ces: EMB source: 2B6.9</wil>	transla L:28107 clone E	ated 74; 732B	com GB/EMBL/DDBJ	22; CESP:F32B6.9
, , , , , , , , , , , , , , , , , , , ,	1003: 42/4		141/2;	176/3;	73; 200/3; 290/3; 332/1	

0

```
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4166-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Species: Lactobacilius case;
C. Date: 22 Nov-1993 #sequence_revision 03-Aug-1995 #text_change 19-Jan-2001
C. Accession: S30597
R.Klugbauer, N.; Ludwig, W.; Baeuerlein, E.; Schleifer, K.H.
Syst. Appl. Microbiol. 15, 323-330, 1992
A.Title: Subunit beta of adenosine triphosphate synthase of Pectinatus frisingensis a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein PA3421 [imported] - Pseudomonas aeruginosa (strain PA6 C; Species: Pseudomonas aeruginosa (strain PA6 C; Species: Pseudomonas aeruginosa (strain 15-Sep-2000 #text_change 31-Dec-2000 (strain A8218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE004763; GB:AE004091; NID:g9949556; PIDN:AAG06809.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Molecule type: DNA_A.Residues: 1-470 <KLUSA.RESIGUES: 1-470 <KLUSA.RESIGUES: 1-470 <KLUSA.RESIGUES: 1-470 <KLUSA.RESIGUES: NID:943971; PIDN:CAA45840.1; PID:943972 C:Superfamily: H-transporting ATP synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                A:Cross-references: GB:AE005673; NID:913425285; PIDN:AAK25511.1; GSPDB:GN00148
C:Genetics:
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H+ transporting ATP synthase (EC 3.6.1.34) beta chain - Lactobacillus casei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.5%; Score 37; DB 2; Length 766; Best Local Similarity 62.5%; Pred. No. 51; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 36; DB 2; Length 456; 66.7%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Experimental source: strain PAOl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Thes 6; Conserva
                                                                                                                                                                                                                                                                                                                    A; Residues: 1-766 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-456 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 OPINDGNGL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    759 QPVDDGEG 766
                                                                                                                                                                                                                                                               preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                        C; Accession: C87689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A83218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S30597
                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CC3549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: PA3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
Reference number: 217011; MUID:97271300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Res. 8, 205-213, 2001
Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
Reference number: AB1807; MUID:21595285; PMID:11759840
Accession: AE2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
akazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Irology 229, 381-399, 1997
Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                               ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:BA000019; PIDN:BAB74199.1; PID:917131592; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U75930; NID:92934903; PIDN:AAC59020.1; PID:91911267
                                                                                                                                                                                                                                                                                                                                                         /pothetical protein 21 - Orgyia pseudotsugata nuclear polyhedrosis virus
Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
:Accession: T10290
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rboxyl-terminal proteinase [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                 Score 40; DB 2; Length 413; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 5
7689
3P-dependent malic enzyme [imported] - Caulobacter crescentus species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.6%; Score 38; DB 2; Length 627;
87.5%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%; Score 37; DB 2; Length 428; 75.0%; Pred. No. 28;
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: carboxyl-terminal processing proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                             100.0%; Pred. No. v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Experimental source: strain PCC 7120
                                                 81.6%;
                                                                          Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-627 <AHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 1-428 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 PLDDGSGL 354
                                                                                                                                                                                                                 384 PIDDGKG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11111 11
25 PIDDGAGL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PIDDGKGL 9
                                                                                                                                                          2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: AE2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T10290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: all2500
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

```
hypothetical protein ytcG - Bacillus subtilis
Nyltranate names: hypothetical protein X (dnaB 5' region)
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Species: Bacillus subtilis
C.Caccession: D69989; Az680
C.Accession: D69989; Az680
C.Accession: D69989; Az680
C.Accession: D69989; Az680
C.Accession: D69989; Az680
C.Authors: Emmerson, P.T. Entland, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzl, A.; Galical, A.; Hibert, H.; Holsappel, S.; Horner,
A.Authors: Lauber
J.; Harvod, C.R.; Henaut, A.; Hibert, H.; Holsappel, S.; Hosnow, S.; Hollo,
Nocetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Kurita, X.; Lapidus, A.; Lardin
A.Authors: Lauber
J.; Annakoshl, A.; Tanaka, T.; Terpstra, P.; Scklaguchi, J.; Sakowska, A.; Sakouchi, M.; Tanaka, H.; Topstra, P.; Tognoni, A.; Tosato, V.; Poll, J.
A.Authors: Solniedr, S.; Schroeter, R.; Socifone, F.; Scklaguchi, J.; Sakowska, A.; Sakouchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy
A.Authors: Solniedr, S.; Schroeter, R.; Socifone, F.; Scklaguchi, J.; Sakowska, A.; Sakouchi, M.; Tanakoshi, A.; Tanaka, H.; Topstra, P.; Topnoni, A.; Tosato, V.; Uchiy
A.Authors: Socione D6989
A; Status; preliminary, nucleic acid sequence of the Gram-positive bacterium Bacillus subtil
A.Accession: D6989
A; Status; preliminary, nucleic acid sequence not shown
A; Reference number: A6980; MUD:98044033
A; Cross-references: GB:29918; GB:AL009126; NID:9253200; PIDN:CAB14860.1; PID:92635
A; Treference number: A94709; MUD:98126; A; Tanaka, T.; Sueoka, N.
A; Reference number: A94709; MUD:8718226
A; Accession: A94800.1; PID:921825
A; Cross-references: GB:29183; NID:9142862; PIDN:AAA22403.1; PID:9469267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein yycp - Bacillus Subtilis

C;Species: Bacillus subtilis

R;Kunst, F; Oqsawara N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be

C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

Nature 390, 249-256, 1997

A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

N; Bature 30, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Funa, S.; Galizzi, A.; Ga

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

R; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porter,

N; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scan

A; Authors: Schleich S.; Schroeter, R.; Scoffone, F.; Sekiguchi, A.; Tosaro, V.; Uchiy.

T; Winters, D.; Wipat, A.; Yanamanoto, H.; Tampane, K.; Yasumoto, K.; Yata, K.; Yoshid

A; Ruthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A; Reference number: A69580; MUDD: 98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 152;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ytcG
C;Superfamily: conserved hypothetical protein HI0943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 62.5%;
Matches 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 PVDDGKSI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: C83339 ... Erwin, A.L.; Mizoquchi, S.D.; Warrener, P.; Hickey, M.J.; Br diam, S.; Yuan, Y.; Brody, E.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, a. Lory, S.; Olson, M.V. ature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
:Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-5627 <STO>
Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05850.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:AL022374; PIDN:CAA18516.1; GSPDB:GN00070; SCOEDB:SC5B8.08
                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Species: Streptomyces coelicolor
:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                            Gaps
;Keywords: ATP biosynthesis; hydrolase; nucleotide binding; P-loop
;155-162/Region: nucleotide-binding motif A (P-loop)
;181-350/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; Ubmitted to the EMBL Data Library, April 1998; *Reference number: 221571 *Accession: T35192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5627;
                                                                                                                                                                       73.5%; Score 36; DB 2; Length 470; 66.7%; Pred. No. 48; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5%; Score 36; DB 2; Length 744; 62.5%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; I
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               robable ABC transporter · Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 87.5%
T; Conservative
                                                                                                                                                                                                        Local Similarity 66.7
Nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
5, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-744 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: SCOEDB:SC5B8.08
                                                                                                                                                                                                                                                                                                                                                                               98 DPIDDGEAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5280 PIDDKKGL 5287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 EPLEDGRG 348
                                                                                                                                                                                                                                                                                                          1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T35192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: C83339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Gene: PA2462
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Genetics:
                                                                                                                                                                                                                                     Matches
```

۵ >

```
DB 2; Length 400;
                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                          63;
                                               71.4%; Score 35; 71.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A: Experimental source: strain Bristol N2
                      Query Match
Best Local Similarity //...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-626 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       579 EPINDGKFL 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |||||:|:
66 EVIDDGRGM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: F35D11.2
                                                                                                                                                                                                       42 PVEDGKG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                     2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: G82078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: VC2431
                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, J. Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; ience 294, 2323-2328, 2001
Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum Reference number: A97359; PMID:11743194
                                                            Residues: 1.1387 - KUN>
Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16064.1; PID:92636574
Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: AF3134

Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I age, G.; Gillet, W.; Ednant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romeco, P.; Zhang, S.
Hence 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isopropylammelide isopropyl amidohydrolase (imported) - Agrobacterium tumefaciens (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. Reference number: Ab2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE008689; PIDN:AAL45492.1; PID:q17743200; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross:references: GB:AE007870; PIDN:AAK88752.1; PID:915158494; GSPDB:GN00170
                        Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Agrobacterium tumefaciens
Date: 11.Jan-2002 #sequence_revision 11.Jan-2002 #text_change 11.Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Agrobacterium tumefaciens
Date: 22-Oct.2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'drolase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                         Ouery Match
71.4%; Score 35; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 2; Length 397; 71.4%; Pred. No. 63; 0; Indels tive 2; Mismatches 0; Indels
                                                                                                                                                                        Gene: yycP
Superfamily: Bacillus subtilis hypothetical protein yycP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: Atu4698
Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Map position; linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-397 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-400 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                       185 PTDDGKG 191
                                                 Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 PVEDGKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                     2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PIDDGKG 8
Accession: D70090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: F98153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: F98153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: AF3134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: AGR_L_364
```

```
A;Wolecule type: DNA
A;Residues: 1-614 <FUL>
A;Cross-references: EMBL:U29381; NID:9868214; PID:9868216; PIDN:AAA68749.1; CESP:F35D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:AE004312, GB:AE003852, NID:99656995, PIDN:AAF95574.1, GSPDB:GN
A,Experimental source: serogroup 01; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 topoisomerase IV, chain B VC2431 [imported] - Vibrio cholerae (strain N16961 serogrou
ö
                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F35D11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #seguence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82078
Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 35; DB 2; Length 614; 77.8%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.4%; Score 35; DB 2; Length 626; 66.7%; Pred. No. 1e+02; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 16/2; 105/3; 172/1; 236/2; 341/3; 373/2; 391/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBi. Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F35Dll.
A;Reference number: 218487
A;Accession: T16268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
```

Search completed: August 6, 2002, 17:05:16 Tob time: 918 sec

```
445549 bacillus su
P20083 escherichia
P31598 mus musculu
P21856 bos taurus
P21856 bos taurus
P21856 bos taurus
P21856 bos taurus
P21856 bomo sapien
P41150 homo sapien
P41150 homo sapien
P41150 homo sapien
P41150 homo sapien
P41150 bombyx mori
P31180 buman cytom
P44569 human cytom
P44569 human wir
P44613 homo sapien
P44117 autographa
                                               August 6, 2002, 17:07:35 ; Search time 32.88 Seconds (without aliynments) 10.598 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                          orgyia pseu
lactobacill
                                                                                                                                                                                                                                                                                                                                         085138 salmonella
045435 caenorhabdi
                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                105224
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                               otal number of hits satisfying chosen parameters:
                                                                                                                                              105224 seqs, 38719550 residues
                                                                                US-10-020-139-2_COPY_115_123
                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 ATPB_LACCA
YTCG_BACSU
PARE_ECOLI
PARE_SALTY
GD1A_MOUSE
GGPP_NEUCR
GD1A_HOWN
GD1A_CANFA
GD1A_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNC_COXBU
VG15_BPT4
RL5_BOMMO
GSPK_AERHY
XYNA_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RL28_HUMAN
RL28_MOUSE
A16_ANOGA
                                                                                                                                                                                                                                                                                                                                        PLSX_SALTY
YV4Q_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENV_HV1C4
DNM1_CHICK
RRPL_HANTV
RRPL_PUUMH
RT67_HUMAN
LEF1_NPVAC
HO2_RABIT
                                 4 protein - protein search, using sw model
                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MK06_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RU17_DROME
                                                                                                                                                                                                                                                                                                                                                        Y023_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXON_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNTD_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTR3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                            GD1A_KAT
                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                inimum DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                           Ost-processing: Minimum Match 0%
                                                                                                                                                                                                                                            SwissProt_40:*
                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                   1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                itle:
erfect score:
                                                                                                                     coring table:
                                                                                                                                                                                                                                                                                                                                                        tabase:
                                                                                                                                               sarched:
                                                                                                     ednence:
                                                  : uo ur
                                                                                                                                                                                                                                                                                                              ssult
```

34 32 65.3 315 1 H02_MNI 35 32 65.3 315 1 H02_MNI 36 32 65.3 315 1 H02_MNI 37 25 65.3 316 1 H02_MNI 38 32 65.3 316 1 H02_MNI 39 32 65.3 360 1 NRTB_RHOCK POPE 40 32 65.3 661 1 DHAM_YEBAT PRAFT 41 32 65.3 661 1 DHAM_YEBAT PRAFT 42 32 65.3 61 1 NJOF_YEBAT PRAFT 43 32 65.3 819 1 NJOF_YEBAT PRAFT 44 32 65.3 819 1 NJOF_YEBAT PRAFT 45 32 65.3 819 1 NJOF_YEBAT PRAFT 46 08218

. . .

```
STANDARD;
                                                                                                                                                                           NCBI_TaxID=164623;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 PIDDGAGL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                             Rohrmann G.F.
         Y023_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                           010282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endities and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensee(sb-sib.ch).
                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                   Pfam. PF02504; FA.synthesis; 1.
Fatty acid biosynthesis; Phospholipid biosynthesis; Complete proteome.
SEQUENCE 359 AA; 38716 MW; ADD01BA971D5ECD8 CRC64;
There are no restrictions on ma as its content is in no
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 413; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                 89.8%; Score 44; DB 1; Length 359; 77.8%; Pred. No. U.31;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-201 (Rel. 40, Last annotation update)
Hypothetical 49.0 kDa protein F32B6.9 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 413 AA; 48965 MW; A66E69AB3C78790B CRC64;
                                                                                                                                                                                                                                                                                                                  Pred. No. 0.31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.6%; Scor.
100.0%; Pred. No. 2...
     the European Bioinformatics Institute.
                                                                                                             EMBL; AF044668; AAC38647.1; ALT_INIT.
EMBL; AE008751; AAL20121.1; -.
EMBL; AL627269; CAD08316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                EMBL; AL627269; CAD08316.1; -. StyGene; SG10682; plsx. InterPro; IPR003664; FA_synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR000615; Worm_fam_8.
Pfam: PF01062; Worm_family_8; 1.
Probom: PD002802; Worm_fam_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z81074; CAB03043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE09864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                        345 EPLDDGKGV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; F32B6.9;
                                                                                                                                                                                                                                                                                                                                                                     1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 PIDDGKG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YV4Q_CAEEL
                                                                                                                                                                                                                                                                                                   Query Match
```

40_CAEEL

SULT 3

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klugbauer N., Ludwig W., Bauerlein E., Schleifer K.H.; "Subunit beta of adenosine triphosphate synthase of Pectinatus frisingensis and Lactobacillus casel."; Syst. Appl. Microbiol, 15:323-330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                            Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 73.1 KDA PROTEIN.; 3B81055F4C27F8E4 CRC64;
                                                                                                                                                                                                                                                                                        MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.6%; Score 38; DB 1; Length 657;
87.5%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. 
 -!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                            01.NOV-1997 (Rel. 35, Created)
16.cCT-2001 (Rel. 40, Last sequence update)
16.cCT-2001 (Rel. 40, Last annotation update)
Hypothetical 73.1 kDa protein precursor (ORF21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TTPB_LACUA STANDARD; PRT; 470 AA. 003234; 01-007-1993 (Rel. 27, Created) 01-00T-1993 (Rel. 27, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP synthase beta chain (EC 3.6.3.14).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 18 657 H
SEQUENCE 657 AA; 73128 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U75930; AAC59020.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactobacillus casei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 7; Conserv
```

```
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PARE OR NFXD OR B3030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Springer A.L., Schmid M.B.;
Nucleic Acids Res. 21:1805-1809(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit structure, and subunit intera
J. Biol. Chem. 268:24481-24481(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT QUINOLONE-RESISTANT HIS-445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91004247; PubMed=2170028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93261812; Pubmed-8388096;
Brotherton P.M., Barth P.T.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94043292; PubMed=8227000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97135236; PubMed=8980775
                                                              EMBL; AF008220; AAC00357.1; -.
                                                                                   Z99118; CAB14860.1; -. M15183; AAA22403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-602 FROM N.A.
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62...
Best Local Similarity 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peng H., Marians K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 63:393-404(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MC1655;
                                                                                                                                                                                                                                                                                                                                                                            18 PVDDGKSI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                      2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARE_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                      EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARE_ECOLI
                                                                                                                                                                                                                                                                                                                                                                            q
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE BUBUNITS: ALPHA(3), BETAMA(1), DELTA(1), EPSILON(1), CF(0) HAS THREE MAIN SUBUNITS: A, B AND C, SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lapidus A., Galleron N., Sorokin A., Ehrlich S.D., "Sequencing and functional annotation of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoshino T., McKenzie T., Schmidt S., Tanaka T., Sueoka N.;
"Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for DNA replication initiation and membrane attachment.";
Proc. Natl. Acad. Sci. U.S. A. 84:653-657(1987).
-: SIMILARITY: BELONGS TO THE UPF0168 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 36; DB 1; Length 470; 66.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
2258AF44C6DE13FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; ATP synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     IPR000194; ATPase_alpha_beta.
                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00006; ATP-synt_ab; 1.
Pfam, PF0386; ATP-synt_ab.; 1.
Pfam, PF02894; ATP-synt_ab. N; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
                                                                                                                                                                                                                                                                                             HSSP; P07677; 1SKY.
InterPro; 1PR004100; ATP-synt_ab_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98048467; Pubmed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168 / PY79;
MEDLINE=87118226; PubMed=3027697;
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000793; ATPASE_AB_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 AA; 51457 MW;
                                                                                                                                                                                                                                                     EMBL; X64542; CAA45840.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-152 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein ytcG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrogen ion transport.
NP_BIND 155 162
                                                                                                                                                                                                                                                                        S30597; S30597.; P07677; 1SKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 DPIDDGEAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTCG_BACSU
Q45549;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESULT 5
TCG_BACSU
  OUDDOOCHBAXXARBAXAEBAXXCOOO
```

```
Kato J.-I., Nishimura Y., Imamura R., Niki H., Hiraga S., Suzuki H.;
"New topoisomerase essential for chromosome segregation in E. coli.";
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Escherichia coli topoisomerase IV. Purification, characterization,
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quinolone resistance locus nfxD of Escherichia coli is a mutant
                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breines D.M., Ouabdesselam S., Ng E.Y., Tankovic J., Shah S.,
Soussy C.J., Hooper D.C.;
                                                                                                                                    71.4%; Score 35; DB 1; Length 152; 62.5%; Pred. No. 7.4; 1:ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                       SEQUENCE OF 588-630 FROM N.A., AND CHARACTERIZATION.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are not restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-S.typhimurium; STRAIN=LT2;
MEDLINE-93261812; PubMed=8388096;
Spřinger A.L., Schmid M.B.;
"Molecular characterization of the Salmonella typhimurium parE gene.";
Nucleic Acids Res. 21:1805-1809(1993).
                                                                                                                                  PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> H (IN QUINOLONE-RESISTANT STRAIN
allele of the parE gene encoding a subunit of topoisomerase IV.", Antimizorb. Agents Chemocher. 41.175-179(1997).
-!- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00177; TOPO1SOMERASE_II; 1. Isomerase; Topoisomerase; ATP-binding; Antibiotic resistance;
                                                                                                                                                             OF A CIRCULAR DNA MOLECULE.
SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE.
SIMILARITY: BALONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.4%; Score 35; DB 1; Length 630; 66.7%; Pred. No. 33; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 AA; 70243 MW; 3F83D108BC1C6A41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-Opolsomerase IV subunit B (EC 5.99.1.-).
PARE OR STM3181 OR STY3359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecogene, EG10687; parE. InterPro; IPR00228, DNA_topoisoII. InterPro; IPR001241; DNA_topoisoII. InterPro; IPR001341; DNA_topoisoII. InterPro; IPR001364; HATPase_c. Pfam; PF00986; DNA_tyraseB_C; I. Pfam; PF0024; DNA_topoisoII; I. Pfam; PF002518; HATPase_C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRO0418; TPI2FAMILY.
ProDom; PD000616; DNA_topoisoII; 1.
ProDom; PD149633; DNA_gyraseB_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M58409; AAA24298.1; ALT_SEQ.
EMBL; U28377; AAA63198.1; --
EMBL; AE000385; AAC76066.1; --
EMBL; L22026; AAC36841.1; --
PIR; B36075; B36075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DH161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-MAR-2002 (Rel. 41, Last segu
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00387; HATPase c;
SMART; SM00433; TOP2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1AJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 EVIDDGRGM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P06982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARE_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULT 7
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                            DECEDS: Lyphi: STRAIN-CT18;
MEDLINE-2154947; PubMed-11677608;
MEDLINE-2154947; PubMed-11677608;
MEDLINE-2154947; PubMed-11677608;
MEDLINE-21549497; PubMed-11677608;
MEDLINE-21549497; PubMed-11677608;
MEDLINE-21549497; PubMed-11677608;
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Elaker S., Basham D., Berooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davis R.M., Dood L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Ouall M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
Whitehead S., Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V -> M (IN TS MUTANTS PAREZOG & PARE374).

G -> S (IN TS MUTANT PARE377).

V -> Q (IN TS MUTANT PARE493).

V -> Q (IN REF. 1).

T -> P (IN REF. 1).

A -> R (IN REF. 1).

7 PZPCCZSEB830019 CRC64;
                                                                                               McClelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                              Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY. PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF A CIRCULAR DNA MOLECULE.
-!- SUBUNIT: COMPOSED OF TWO SUBUNITS: PARC AND PARE.
-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                               SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7%; Pred. No. 33. Matches 6; Consormation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Topoisomerase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD149633; DNA_gyraseB_C; 1.
SMART; SM00387; HATPASSE_C: 1.
SMART; SW00433; TOP2C; 1.
PROSITE; PS00177; TOP0ISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stydene: SG10277: parE.
InterPro: IPR002288: DNA_gyraseB_C.
InterPro: IPR001241: DNA_topoisoll.
InterPro: IPR003594; HATPase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000616; DNA_topoiso11; 1.
ProDom; PD149633; DNA_gyraseB_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L05544; AAA27182.1; -.
EMBL; AE008846; AAL22055.1; -.
EMBL; AL627277; CAD03013.1; -.
PIR; S33711; S33711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam; PF02518; HATPase_c; 1
PRINTS; PR00418; TPI2FAMILY
                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583
305
333
383
383
630 AA;
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
```

```
1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDI).
GDI1 OR RABGDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDIA_BOVIN
P21856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDIA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (GGPPSASE)
(Geranylgeranyl diphosphate synthase) [Includes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
1-0cT-1996 (Rel. 34, Last Sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1)
                                                                                                                                                                                                                                                                                                                                               MEDLINE-94217740; Dubmed-7513052;
Shisheva A., Zuedhof T.C., Czech M.P.;
"Cloning, characterization, and expression of a novel GDP
dissociation inhibitor isoform from skeletal muscle.";
Mol. Cell. Biol. 14:3459-3468/1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 34; DB 1; Length 323; 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 1 SEQUENCE 323 AA; 36601 MW; 141551B65852578E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBSEQUENT BINDING OF GTP TO THEM. SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                        323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred ...
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD, MGI:99846; Gdil.
InterPro; IPR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U07950; AAB16907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GND.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BALB/C; T15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTPase activation.
                                          66 EVIDDGRGM 74
                                                                                                                                                                                                                                                                                                 NCB1_TaxID=10090;
           1 EPIDDGKGL 9
                                                                                                                                                                                                                                   OR RABGDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 EPIDDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPIDDG 6
                                                                                                                     GDIA_MOUSE
P50396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPP_NEUCR
P2432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSULT 9
3PP_NEUCR
                                                                                                       DIA_MOUSE
                                        Ω
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWBL outstarion the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as iony as its conversion modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1) (SMG P25A
                                                                                                                                                                                                                                                                                                                                                                                                         Carattoli A., Romano N., Ballario P., Morelli G., Macino G.,
"The Neurospora crassa carotenoid biosynthetic gene (albino 3)
reveals highly conserved requons among prenyltransferases.",
J. Biol. Chem. 266:5854-5859(1991).
-!- FUNCTION: CATALYZES THE TRANS-ADDITION OF THE THREE MOLECULES OF
IPP ONTO DMAPP TO FORM CRANYLGERANYL PYROPHOSPHATE.
-!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate.
-!- CATALYTIC ACTIVITY: Geranyl diphosphate.
-!- CATALYTIC ACTIVITY: Geranyl diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -diphosphate + trans,trans-farmesyl diphosphate.
-t-CATALYITC ACTIVITY: Trans-trans-farmesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.
-t- PATHWAY: CAROTENOID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10); Farnesyltranstransferase (EC 2.5.1.29)].
AL-3 OR ALBINO-3.
                                                                                                                                Eukaryota: Fungi: Ascomycota: Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00148; polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
PROSITE; PS00723; POLYPRENYL_SYNTHET_1: 1.
Carotenoid biosynthesis; Isoprene biosynthesis; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE FPP/GGPP SYNTHETASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.4%; Score 34; DB 1; Length 428; Best Local Similarity 75.0%; Pred. No. 35; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY, 7989DEEABD8E360F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S15662; S15662.
InterPro; IPR000092; Polyprenyl_synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=74-OR23-1A;
MEDLINE=91170267; PubMed=1826006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 AA; 47887 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U20940; AAC13867.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                    Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 EDIDDGRG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
```

. 0

```
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the Loropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            "Molecular cloning and characterization of a novel type of regulatory protein (GDI) for smg p25A, a ras p21-like GTP-binding protein."; Mol. Cell. Biol. 10:4116-4122(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: REGULATES THE GDF/GTP EXCHANGE REACTION OF MOST RAB PROPIEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W., Feng Y., Chen D., Wandinger-Ness A.;
"Rebli is required for trans-golgi network-to-plasma membrane
transport and a preferential target for GDP dissociation inhibitor.";
Mol. Biol. Cell 9:3241-3257(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
MEDLINE-90318376; PubMed-2115118;
Matsui Y., Kikuchi A., Araki S., Hata Y., Kondo J., Teranishi Y.,
                                                                                                                                                                                                                                                                                                    MEDLINE=96196507; PubMed=8609986; Schalk I., Zeng K., Wu S., K., Stura E.A., Matteson J., Huang M., Tandon A., Wilson I.A., Balch W.E.; "Structure and mutational analysis of Rab GDP-dissociation inhibitor."; 18142-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 447;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTPase activation; 3D-structure.
SEQUENCE 447 AA; 50565 MW; 69C68B03BDC1BA3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS).
                                                                                                                                                 SIMILARITY TO CHOROIDERAEMIA PROTEIN.
                                                                                                                                                                      MEDLINE=91270365; PubMed=1904992; Fodor E., Lee R.T., O'Donnell J.J.; "Analysis of choroideraemia gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.48; Scc...
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99019719; Pubmed=9802909; Chen W., Feng Y., Chen D., Wanding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002005; Rab_GDI_REP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D90103; BAA14134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00891; RABGDIREP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                          Nature 351:614-614(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1GND; 12-FEB-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A35652; A35652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11111
388 EPIDDG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EPIDDG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIA_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULT 11
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM.

-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-! SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1) (XAP-4).
GDII OR RABGDIA OR XAP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an Xq28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishimura N., Goji J., Nakamura H., Orita S., Takai Y., Sano K.; "Cloning of a brain-type isoform of human Rab GDI and its expression in human neuroblastoma cell lines and tumor specimens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96311563; PubMed=8733135;
Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,
Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95152170; Pubmed-7849400; Sediacek Z., Konecki D.S., Korn B., Klauck S.M., Poustka A.; Sediacek Z., Konecki D.S., Korn B., Klauck S.M., Poustka A.; "Evolutionary conservation and genomic organization of XAP-4, a located gene coding for a human rab GDP-dissociation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 34; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA; 50520 MW; 10280DAD33E4BCD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96062207; PubMed=7585614;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002005; Rab_GDI_REP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G6PD loci.",
Hum. Mol. Genet. 5:659-668(1996).
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer Res. 55:5445-5450(1995).
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF027360; AAD04246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome 5:633-639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00891; RABGDIREP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDI;
                                                                                                                                                                                                                                                                                                                                                                                                          1GND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTPase activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 EPIDDG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P31150; P50394;
                                                                                                                              INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EPIDIG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDIA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D'Urso M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98282090; PubMed-9620768; D'Adamo P., Menegon A., Lo Nigro C., Grasso M., Gulisano M., Tandanini F., Blenvenu T., Gedeon A.K., Costra B., Wu S.-K., Tandon A., Valtorta F., Balch W.E., Chelly J., Toniolo D.; "Mutattains in GDII are responsible for X-linked non-specific mental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98334551; PubMed-9668174; Blenvenu T., Des Porties V., Saint Martin A., McDonell N., Billuart P., Carrie A., Vinet M.-C., Couvert P., Toniolo D., Ropers H.-H., Moraine C., van Bokhoven H., Fryns J.-P., Kahn A., Beldjord C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Non-specific X-linked semidominant mental retardation by mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95359978; PubMed-7543319; Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A.; Expression patterns of two human genes coding for different rab GDP-dissociation inhibitors (GDIs), extremely conserved proteins involved in cellular transport.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.; "Microsequences of 145 proteins recorded in the two-dimensional gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DISEASE: DEFECTS IN GDI1 ARE THE CAUSE OF X-LINKED NON-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENTAL RETARDATION (XLMR). SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a Rab GDP-dissociation inhibitor.";
Hum. Mol. Genet. 7:1311-1315(1998).
-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBSEQUENT BINDING OF GTP TO THEM.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: BRAIN; PREDOMINANT IN NEURAL AND SENSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein database of normal human epidermal keratinocytes."
                                                                                                                   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mol. Genet. 4:701-708(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X79354, CAA55909.1; -. EMBL, X79355, CAA55909.1; JOINED. EMBL, X79356, CAA55909.1, JOINED. EMBL, X79358, CAA55909.1, JOINED. EMBL, X79358, CAA55909.1, JOINED. EMBL, X79359, CAA55909.1, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T1SSUE=Keratinocytes;
MEDLINE=93162043; PubMed~1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lectrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet. 19:134-139(1998).
                                                                                                                                                                                                        SEQUENCE OF 143-181 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 328-436 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT XLMR PRO-423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 349-361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT XLMR PRO-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet.
                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retardation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUES.
                                        FISSUE=Lung
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L -> P (IN XLMR; CAUSES REDUCED BINDING AND RECYCLING OF RAB3A).

/FIG-VAR (08130.

R -> P (IN XLMR).

/FIG-VAR_008131.

D -> G (IN REF. 2).

N -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishimura N.; Nakamura H., Takai Y., Sano K.; Mblecular cloning and characterization of two rab GDI species from rat brain. brain-specific and ubiquitous types."; J. Biol. Chem. 269:14191-14198 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDIA_RAT STANDARD; PRT; 447 AA. p5039; 09R274; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) 01-0CT-2001 (Rel. 40) Last annotation update) 01SCC-10CT-2001 (Rel. 40) Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.4%; Score 34; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE—94217740; PubMed=7513052;
Shisheva A., Suedhof T.C., Czech M.P.;
"Cloning, characterization, and expression of a novel GDP
dissociation inhibitor isoform from skeletal muscle.";
Mol. Cell. Biol. 14:3459-3468(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFD -> GTY (IN REF. 2).

G -> V (IN REF. 5).

H -> Q (IN REF. 5).

D -> G (IN REF. 5).

F -> S (IN REF. 2).

F -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTPase activation; Disease mutation.
X79360; CAA55909.1; JOINED.
X79364; CAA55909.1; JOINED.
X79361; CAA55909.1; JOINED.
X79362; CAA55909.1; JOINED.
X79363; CAA55909.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94245743; PubMed-8188702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                               L44140; AAA92648.1; -. BC000317; AAH00317.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Aarhus/Ghent-2DPAGE; 8408; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50582 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                        U14623, AAA21558.1; -. D45021; BAA08078.1; -. L05086; AAC15851.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00891; RABGDIREP
                                                                                                                                                                                    X79353; CAA55908.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
34
34
34
34
40
44
42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409
416
442
447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        JGND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 EPIDDG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPIDDG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 300104; -
                                                                                                                                                                                                                                                                                                                                                                                                        P21856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 309541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                            EMBL;
EMBL;
                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                  EMBL;
                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDIA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NA COOR WAS A STATE OF THE STAT
```

ó

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase 6 (EC 2.7.1.-) (Extracellular signal-regulated kinase 3) (ERK-3) (MAP kinase isoform p97) (p97-MAPK).
                                                                                                                                                                                          -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal skeletal muscle;
MEDLINE=95059049; PubMed=7969157;
MACH A.X., Zhao Y., Moller D.E., Filer J.S.;
"Cloning and characterization of p97MAPK, a novel human homolog of rat ERK-3.";
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                           Caillol N., Pasqualini E., Lloubes R., Lombardo D.; "Impairment to file salt-dependent lipase secretion in human panoreatic tumoral SOJ-6 cells."; Description of 19:628-647(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%; Score 34; DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D -> Y (IN REF. 1).
G -> S (IN REF. 2).
S -> P (IN REF. 2).
; 58384671991DF793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; Pred. ....
                                                                                                                                                                                                                                                   SUBSEQUENT BINDING OF CTP TO THEM.
                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 14:8202-8211(1994).
                                                   MEDLINE=20453283; PubMed=10996854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002005; Rab_GD1_REP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97030046; PubMed=8875998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF130987; AAD25536.1; -.
HSSP; P21856; 1GND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50536 MW;
SEQUENCE OF 81-439 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X74402; CAA52413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00891; RABGDIREP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.99
230
330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB16909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAPK6 OR PRKM6 OR ERK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00996; GDI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPase activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I_TaxID=9606;
                                 TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 EPIDDG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPIDDG 6
                                                                                                                                                                                                                                                                                                                                                                                             INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MK06_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frigerio J.-M., Dagorn J.C., Iovanna J.L.;
"Cloning, sequencing and expression of the L5, L21, L27a, L28, S5, S9, S10 and S29 human ribosomal protein mRNAs.":
Biochim. Biophys. Acta 1262:64-68(1995).
-:- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 34; DB 1; Length 721; 71.4%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
DAA3AAA9B98BB31F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
Meloche S., Beatty B.G., Pellerin J.;
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95290496; PubMed=7772601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82680 MW;
                                                                                                                                                                                                                                                                                                    EMBL; X80692; CAA56709.1; -.
                                                                                                                                                                                                                                                                                                                 EMBL; L77964; AAA98769.1; -...
HSSP; P27703; 1ERK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60S ribosomal protein L28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; SMART; SM00220; S TKC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 645 EPVEDGK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EPIDDGK 7
                                                                                                                                                                                                                                                                                                                                                 MIM; 602904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL28_HUMAN
P46779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KL28_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  EMBL; U14969; AAA85657.1; -.
MIM; 603638; -.
InterPro; IPR002672; Kibosomal_L28e.
Fram; PF01778; Kibosomal_L28e; 1.
ProDom; PD010767; Kibosomal_L28e; 1.
Ribosomal protein.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 136 AA; 15630 MW; 6551B12C473D2342 CRC64;
```

ó:

0; Gaps

2; Indels

Ouery Match 67.3%; Score 33; DB 1; Length 136; Best Local Similarity 66.7%; Pred. No. 16; Matches 6; Conservative 1; Mismatches 2; Indels

earch completed: August 6, 2002, 17:07:36 ob time: 878 sec

11 || iii: 51 EPAADGKGV 59 1 EPIDDGKGL 9

> 0

```
092643 rhizoblum m
0991vi4 pseudomonas
06995 streptomyce
09fcu3 neisseria m
091120 pseudomonas
038126 human immun
038236 human immun
                                                                                August. 6, 2002, 17:09:30 ; Search time 111.35 Seconds (without alignments) 13:983 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9w5r8 drosophila
Q9v3z6 drosophila
Q9sfe7 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09a212 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  030968 nostoc punc
Q93cc8 staphylococ
Q9niu2 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96dr5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                           562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                         otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             562222 seqs, 172994929 residues
                                                                                                                                           US-10-020-139-2_COPY_115_123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                       M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W5R8
Q9V3Z6
Q9SFE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9A2L2
Q926D3
Q9HXI4
Q69995
Q9FZU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        038236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BQQ0
Q96DR5
Q30968
Q93CC8
Q93CC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                       SPTREMBL_19:*
: Sp_archea:*
: Sp_bacteria:*
                                                                                                                                                                                                                                                                                                     inimum DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                 ost-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_phage:*
                                                                                                                                                                       1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777.6
                                                                                                                                                         erfect score:
                                                                                                                                                                                                     coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                           atabase :
                                                                                                                                                                         ednence:
                                                                                                                                                                                                                                             earched:
                                                                                     no un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esult
```

17 35 71.4 154 16 098H58 18 35 71.4 258 15 P8480 20 35 71.4 614 50 098E08 21 35 71.4 614 50 008E08 22 35 71.4 614 50 20 008E08 22 35 71.4 614 50 20 008E08 23 35 71.4 629 2 008E08 24 35 71.4 629 2 008E08 25 34 69.4 98 15 008232 29 34 69.4 98 15 008234 31 69.4 98 15 008234 31 69.4 98 15 008234 31 69.4 113 15 008244 31 69.4 113 15 008244 31 69.4 113 15 008244 31 69.4 113 15 008244 31 69.4 113 15 008244 31 69.4 113 15 008E04 31 69.4 443 5 008E04 32 69.4 443 5 008E04 33 69.4 464 10 09E04 34 69.4 464 10 09E04 35 69.4 464 10 09E04 36 69.4 464 10 09E04 37 69.4 464 10 09E04 38 69.4 464 10 09E04 39 69.4 464 10 09E04 30 69.4 464 10 09E04 30 69.4 464 10 09E04 31 69.4 464 10 09E04 32 69.4 464 10 09E04 33 69.4 464 10 09E04 34 69.4 465 5 0E04 35 69.4 465 5 0E04 36 69.4 466 10 0E04 37 69.4 466 10 0E04 38 69.4 466 10 0E04 39 60.4 466 10 0E04 30 60.4 466 30 60.	; 249 AA. ed) sequence update) annotation update)
488888222323232323232323232323333333333	PRT; Created) Last seque
488888222323232323232323232323333333333	222
71.4 71.4 71.4 71.4 71.4 71.4 71.4 71.4	PRELIMINARY; (TrEMBLrel. 19 (TrEMBLrel. 19 (TrEMBLrel. 19 ETORY PROTEIN. (Human).
	PRELI (TrEM (TrEM (TrEM)RETORY
117 35 71.4 20 35 71.4 21 35 71.4 22 35 71.4 23 35 71.4 24 35 71.4 25 34 69.4 26 34 69.4 27 34 69.4 28 35 71.4 29 80.00 10.00.00.00 10.00.00.00 10.00.00.00 10.00.00.00 10.00.00.00 10.00.00.00 10.00.00.00 10.0	96DR5, 1-DEC-2001 (TrEMBLrel 1-DEC-2001 (TrEMBLrel 1-DEC-2001 (TrEMBLrel 1-DEC-2001 (TrEMBLrel AROTID SECRETORY PROTI
RESULT 1 EP 10 P P P P P P P P P P P P P P P P P P	Q96DR5 ID Q96DF AC Q96DF DT 01-DF DT 01-DF DT 01-DF DT 01-DF OS HOMO

```
Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09NIU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09NIU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9W5R8
Q9W5R8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESUL'Y 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9W5R8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
              DDT DDT BEND DDT BEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC AC DIT DIT DIT DIT OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OCT-2001).
Submitted (OCT-2001).
SEMBL, AF432917: AAL28113.1: -.
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campbell E.L., Brahamsha B., Meeks J.C.;
"Mutation of an alternative sigma factor in the cyanobacterium nostoc punctiforme results in increased infection of its symbiotic plant partner, anthoceros punctatus.";
J. Bacteriol. 180:4938-4941(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0\$; Score 49; DB 4; Length 249; Best Local Similarity 100.0\$; Pred. No. 0.28; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.7%; Score 42; DB 2; Length 424; Best Local Similarity 77.8%; Pred. No. 10; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=63737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA; 45830 MW; C1736347D3EFCDA1 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 18.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC29133;
MEDLINE=98406048; PubMed=9733698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | InterPro: | IPR001478; | PDZ. | InterPro: | IPR001478; | PDZ. | InterPro: | IPR005581; | TSPC. | PTM: | PTM: | SMART; | SM00228; | PDZ; | ISMART; | SMART; | SM00245; | TSPC; | I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF022823; AAC45366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOXYL TERMINAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=PAROTID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 EPIDDGKGL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nostoc punctiforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 EPLDDGSGL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S41.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              030968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               030968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q93CC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULT
```

```
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                         Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V., Schlievert P.M.;
Schlievert P.M.;
Staphylococcus aureus pathogenicity island 3 (SaP13).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF410775; AAL04144.1;
Hypothetical protein.
SEQUENCE 152 AA, 18082 MW; 17A63018DE9B9AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                   Query Match 77.6%; Score 38; DB 2; Length 152; Best Local Similarity 87.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.6%; Score 38; DB 5; Length 176; 75.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA: 19791 MW; 73CE21AB75AE80A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Bacieria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIPPEE INTERACTING PROTEIN 6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIP6 OR CG17489.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-IMAGINAL DISCS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 PIDDGKSL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||| |
|8 EPVDDGPG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIP6 PROTEIN,
YIP6 OR CG17489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EPIDDGKG 8
                                                                                                                             STRAIN-COL;
```

```
MEDLINE=CUISOUCS; LONGEGINGS. LIPPW., Hoskins R.A., Gotayne J.D.,
Amanatides P.G., Scherer S.E., Ilp Pw., Hoskins R.A., Galle R.F.,
amanatides P.G., Scherer S.E., Ilp Pw., Hoskins R.A., Galle R.F.,
auton G.C., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.C., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A brandon R.C., Rayers Y. H.C., Blazel R.G., Champer M., Prielifer B.D.,
Wan K.H., Doyle C., Baxter E.G., Hellt G., Champe M., Prielifer B.D.,
Ran K.H., Basu A., An H.-J., Andrews-Pfankoch C. Baldwin D.D.
Ballew K.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
Ballew K.M., Basu A., Baxendale J., Bayrakternyolu L., Beasley E.M.,
Ballew K.M., Basu A., Baxendale J., Bayrakternyolu L., Beasley E.M.,
Bartis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cooler C., Gabriellan A.E., Cons M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
Acient D., Houston K.A., Helman T.J., Hernandez J.R., Heuris M.,
Alaskop P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Heuris M.
Alaskop P., Lei Y., Levitsky A.A., Li J., Li J., Mel M.-H., Ibeywam C.,
Alashi M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Melson D.L.,
Mouston K.A., Murphy B., Murp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.6%; Score 38; DB 5; Length 299; 75.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 AA; Ribosomal_L18p; 1.
299 AA; 34037 MW; 523F50ED67E7841A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09V3Z6 PRELIMINARY; PRT; 2167 AA.
09V3Z6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CK GEME PRODUCT.
CK OR BG:DSO0929.11 OR CG7595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0040061; yip6.
InterPro; IPR001149; Ribosomal_L18p.
                                                                                                                                           STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00861; Ribosomal_L18p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00058; RIBOSOMALLS.
ProDom; PD001394; Ribosomal_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AE002910: AAF45418.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 75.0° nes 6; Conservative
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 EPVDDGPG 140
                                                  Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

```
A Fosler C. Gabriellan AE. Garrell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Ximmel B.E., Kodira C.D., Kraft C., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Parl V., Reese M.G.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spire E., Spradling A.C., Stapleton M., Strong R., Sun S.,
RA Svirskas R., Tector C., Turner R., Verier E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinstong R.,
RA Wang Z.-Y., Wassarman D.A., Weinstong R.,
RA W
                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
A Wan K.H., Doyle C., Baxrer E.G., Helt G., Nelson C.K., Miklos G.L.G.,
A Mari J.F., Adpayani A., An H.-J., Andrews Pfannecch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Burtis K.C., Busam D.A., Burtler H., Cadleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Y, AND CN BW SP,
STRAIN-Y, AND CN BW SP,
MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Hong L., Houston R., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S. Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfelffer B., Poon L., Sequaira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Glibs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Droscophila melanogaster."; science 287:2185-2195(2000).
                                                       Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker S., Rubin G.M.; "An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AE003646; AAF53435.1; -.
EMBL: AE003412; AAF44915.1; -.
Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hong L.,
Palazzolo M., Reese ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Y, AND CN BW SP;
                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                       Ephydroidea; Drc
                                                                                                                                                                                                                           STRAIN~BERKELEY;
```

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Arabidopsis thaliana BAC T26F17 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.6%; Score 38; DB 5; Length 2167; Best Local Similarity 85.7%; Pred. No. 3.5e+02; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2167 AA; 250307 MW; 3C57E34ADDD89A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO1037; SBP_BACTERIAL_1; UNKNOWN_1. PROSITE; PS50002; SH3; 1. SEQUENCE 2167 AA; 250307 MW; 3C57E34ADDDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                             PRINTS, PR00193, MYOSINHEAVY.
ProDom; PD000355, myosin_head; 1.
SMART; SM00195; B41; 2.
SMART; SM0015; 10; 3.
SMART; SM0015; 10; 3.
SMART; SM00139; MYSC; 1.
SMART; SM00139; MYPH4; 2.
SMART; SM00139; MYPH4; 2.
PROSITE: PS50096; 10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                         InterPro; IPR001609; myosin_head.
InterPro; IPR000857; MYTH4.
InterPro; IPR000567; SBE_bac_1.
InterPro; IPR001452; SH3.
                                                                                                                                                   Pfam; PF00612; 1Q; 4.
Pfam; PF0065; myosin_head; 1.
Pfam; PF00784; MyTH4; 2.
Pfam; PF00718; SH3; 1.
                                 InterPro; IPR000299; Band_4.1.
                                                      InterPro; IPR000048; IQ.
                FlyBase; FBgn0000317; ck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Shinn P., Brooks S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  926 EPVDDGK 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EPIDDGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SFE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULT
```

```
SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Li J., Sakano H., Schwartz J., Southwick A.,
Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC013482; AAF16542.1;
EMBL; AC013482; DuF6; 2.
Fram: PF00892: DUF6; 2.
Fram: PF00892: DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAILWATCC 19089 / CB15;
MEDLING-2173698 Pubbed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Ely B.,
Foldby R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Rolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Wamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S. A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.5%; Score 37; DB 10; Length 391; 66.7%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.5%; Score 37; DB 16; Length 766; Best Local Similarity 62.5%; Pred. No. 1.7e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         766 AA; 82539 MW; 7B8E11FEB06577A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS00331; MALIC_ENZYMES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 82;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00515; BPD_transp.
InterPro; IPR01891; Malic_enzyme.
InterPro; IPR002505; PTA_PTB.
Pfam; PF00390; malic; 1.
Pfam; PF01515; PTA_PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADP-DEPENDENT MALIC ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity ov...
6: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter crescentus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 KPVDTGKGL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759 OPVDDGEG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; CC3549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9A2L2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09A2L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9A2L2
```

ö

```
ò
                                                                                                                                                                                                                     .,
0
                                                                                                                                                                                                                                                                              Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barnett M.J., Becker A., Boistard P., Bothe G., Burnester J., Cadieu E., Capela D., Chain P., Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gloux S., Godfrau A., Golfang B., Gouzy J., Gurial M., Hernandez-Lucas I., Hong A. Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portectalle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.; The Composite genome of the legume symbiont Sinorhizobium mellioti." EMBL, AL591786; CAC455081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATC 15692 / PAO1:
STRAIN=ATC 15692 / PAO1:
MEDLINE=20473373 Pubmed-1.0984043;
MEDLINE=20433373 Pubmed-1.0984043;
Stover C. S. A., Phan X.-O. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
NCBL_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.5%; Score 36; DB 16; Length 410; Best Local Similarity 62.5%; Pred. No. 1.3e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE N-ACETYLMURAMOYI-L-ALANIDE AMIDASE AMIC PRECURSOR
TRANSMEMBRANE PROTEIN (EC 3.5.1.28).
Rhizobium meliioti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE004763, AAG06809.1; -.
Hypothetical protein, Complete proteome.
SEQUENCE 456 AA; 50690 MW; BFE2F230EC94F736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Complete protecome.
SEQUENCE 410 AA; 44588 MW; CF55FC972194EB8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA3421.
                                410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                PRT;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=1021;
MEDLINE=21368234; PubMed=11474104;
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 KPVEDGKG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9HYI4
Q9HYI4;
                                                Q926D3;
                              Q926D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESULT 11
9HY14
ESULT
926D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.:
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL022374; CAA18516.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                  0
73.5%; Score 36; DB 16; Length 456; 66.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.5%; Score 36; DB 2; Length 744; Best Local Similarity 62.5%; Pred. No. 2.5e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seeger K., Harris D.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J.; Barrell B.G., Rajandream M.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00005; ABC_tran; 1.
SEQUENCE 744 AA; 76147 MW; 160ED0C5EC8BDD86 CRC64;
                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TTEMBLrel. 07, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1421 AA.
                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21172874; PubMed=11274117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis phage 2120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=3(2);
MEDLINE=97000351; PubMed=8843436;
                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                           Best Local Similarity
                                                                                                                                           141 OPINDGNGL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=132905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 EPLEDGRG 348
                                                                                             1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                    COSMID 5B8
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses
                                                                                                                                                                                                                                                                                         069995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09FZU3;
                                                                                                                                                                                                                                                               069995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09F2U3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORF 4
                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                Matches
                                                                                                                                                                                                                                           069995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FZU3
```

```
STRAIN+ATC 15692 / PAOI:

STRAIN+ATCC 15692 / PAOI:

MEDLINE-20437337; bubMed=10984043;

STORINE-20437337; bubMed=10984043;

STORINE-20437337; bubMed=10984043;

SLOVER C.K. Pham X.-O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOI, an Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Claus H., Stoevesandt J., Frosch M., Vogel U.; "Genetic isolation of meningococci of the electrophoretic type 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.5%; Score 36; DB 16; Lenyth 5627; Best Local Similarity 87.5%; Pred. No. 2.3e+03; Matches 7; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                     73.5%; Score 36; DB 9; Length 1421; 75.0%; Pred. No. 5.2e+02; ative 1; Mismatches 1; Indels
                                                                                      J. Bacteriol. 183:2570-2575(2001).
EMBL; AJ278707; CAC19023.1; -.
Interpres IPR003961; FN_III.
SMART; SMO0060; FN3; I.
SEQUENCE 1421 AA; 153413 MW; 7A17FD4AEB6FA9A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: AE004673, AAG03850.1; -.
InterPro: IPR01899; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 5627 AA; 573167 MW; 2D2A1154C99D3750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Virus.s; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 5627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROTEIN PA2462.
                                                                                                                                                                                                                                                                                                            Query Match 73.5°
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAG PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11:111 |
317 EPVDDGFG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      091120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        038236
```

```
Gaps
                                                  Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J., Vasudevachari M.B., Salzman N.P.;
"Drug resistance during indinavir therapy is caused by mutations in the protease gene and in its Gag substrate cleavage sites.";
J. Virol. 71:666-6670(1997).
EMBL: AF024133; ABB83009.1;
HSSP: P05888: IAAF.
                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                    71.4%; Score 35; DB 15; Length 113; 77.8%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                      NON-TER 113 113
SEQUENCE 113 AA; 12888 MW; 671A99EDZDD5D8B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 6, 2002, 17:09:32
                             STRAIN=PATIENT 5;
MEDLINE=97404676; PubMed-9261388;
                                                                                                                                                            Interpro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              100 EPIDKDKGL 108
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                1 EPIDDGKGL 9
                                                                                                                                                                                                                          Zinc-finger.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time: 934 sec
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                 Matches
ó
```

```
Human parotid secr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein segu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanog
                                                                                                                                 (without alignments)
7.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1998.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2000 DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*/SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*/SIDS1/gogdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1997.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parotid s
PRO1025 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT
                                                                                                             August 6, 2002, 16:52:53 ; Search Lime 138.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/qcgdata/hold-geneseq/genesegp-embl/AA1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Нишап
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                             747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                             US-10-020-139-2_COPY_115_123
49
                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB67420
ABB60369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW60682
AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM25745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW69221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB25765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB66320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB7535
                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                    Inimum DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ost-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                              1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000.0
1000.0
1000.0
1000.0
77.6
77.6
77.6
77.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erfect score:
                                                                                                                                                                                                                                                                        coring table:
                                                                                M protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atabase :
                                                                                                                                                                                                                                                                                                                             earched:
                                                                                                                                                                                                                                  edneuce:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 2 4 2 2 7 2 2 1 1
                                                                                                                     :uo un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tesult
```

Novel human diagno Novel human diagno

ABG24503 ABG29553

Drosophila melanoq

Micromonospora eve Propionibacterium Novel human diagno Propionibacterium S. aureus D-alanin Drosophila melanog smg p25A GDP Disso Drosophila melanog Novel human diagno Human secreted pro Human secreted pro Staphylococcus aur Novel human accreted pro Human secreted pro Propionibacterium Human novel secret Drosophila melanog Novel human diagno A human apoptosis C. pneumoniae prot Thermostable alkal Bacillus sp. xylan Brologically equiv Biologically equiv Biologically equiv	isorder; endocrine disorder; disorder; cancer; human;
296 22 AAU04903 414 22 AAU5477 414 22 AAU5477 282 20 AAW73375 447 12 AAU61020 72 20 AAW7238 445 22 ABB60633 447 22 ABB60633 447 22 ABB60633 112 21 AAG04013 113 21 AAG04013 113 21 AAG01930 144 21 AAG01930 145 22 AAU66394 155 22 AAU66394 168 22 AAU66394 168 22 AAU66394 168 22 AAU66394 168 22 AAU66394 169 22 AAU66394 169 22 AAU66394 164 21 AAB6693 164 22 AAU6639 165 22 AAU6639 166 22 AAU6639 167 22 AAU6639 168 22 AAU6639 169 22 AAU6639 169 22 AAU6639 169 22 AAU6639 169 22 AAU6639 160 22 AAU6639 160 22 AAU6639 160 22 AAU6639 161 22 AAU6040 162 22 AAU6639 163 22 AAU6040 164 22 AAU6040 165 22 AAU6040 166 AAW40046 167 AAW40046 168 29 AAW40049 169 AAW40049 169 AAW40049 169 AAW40049	rotein; 249 AA. entry) ory protein. otein; hPSP; digestive disorder; immune system disorder; immune system tion/Qualifiers 8 e= "signal peptide" 249 e= "mature hPSP" US23522. 0034429. SCI INC.
22 33 34 55 56 56 57 57 57 57 57 57 57 57 57 57	AAW69221 standar. AAW69221 standar. AAW69221; . 16-OCT-1998 (fi Human parotid se Parotid secretor non-immune defen therapy; diagnos Homo sapiens. Key Peptide Protein WO9828420-A1. 02-JUL-1998. 18-DEC-1997; 9 23-DEC-1997; 9 (HUMA-) HUMAN GE
	REGULT A AWG 92 DE A AWG 92 DE AWG 9

```
N-PSDB; AAV44759
```

New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening

Claim 16; Fig 1; 94pp; English.

amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hBSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNN. The protein, or cells expressing it, are used in screening tests to identify specific (anti)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hBSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, hPSP-binding proteins.

249 AA;

.; 0 0; Gaps 100.0%; Score 49; DB 19; Length 249; 100.0%; Pred. No. 0.084; Live 0; Mismatches 0; Indels (9; Conservative }uery Match
3est Local Similarity
4atches 9; Conserv

1 EPIDDGKGL 9

160682

AAW60682 standard; Protein; 249 AA.

AAW60682:

18-SEP-1998 (first entry)

Human parotid secretory protein (HPSP).

secretory tissue; gasirointestinal tissue; HPSP; Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancrealitis; ulcefrative colitis; Crohn's disease; atrophic gastritis. Parotid secretory protein; human; cancer; autoimmune disease;

Homo sapiens.

22-MAY-1998.

97WO-US20651. 07-NOV-1997; 96US-0749288. 14-NOV-1996;

(INCY-) INCYTE PHARM INC.

Goli SK;

Bandman O,

WPI; 1998-297933/26.

N-PSDB; AAV37699

New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or

```
This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or secretory or secretory to astrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Slorgen's syndrome, or prostate, breast, gastrointestinal tract or pancreas, Slorgen's syndrome, allocative colitis, cronk's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP mancler acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may condetect HPSP-encoding sequences (optionally after amplification by PCR) by MPDF diseated and monitoring of disease, but a series of the contains the contains and monitoring of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour; diagnosis; neoplastic disease, neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
beurchal disorder; glial disorder; astrocytal disorder; angiogenic;
hypothalamic disorder; glandular disorder; macrophagal disorder;
epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 49; DB 19; Length 249; ilarity 100.0%; Pred. No. 0.084; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB24069 standard; Protein; 249 AA.
                                                                  Claim 1; Fig 1A-C; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US12252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0141037.
99US-0143048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Baker KP,
gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 epiddgkgl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200053755-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
THE STANDARD STANDARD
```

```
colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioplastomas, and various head and neck tumours). leukaemias and lymphoid malignancles, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC$8342 to AAC$836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC$8365 robresent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth. The PRO polypeptides and nucleotides are useful in the treatment, disponsis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disporters to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alcheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRC212, PRC399, PRC341, PRC535, PRC649, PRC917, PRC689, PRC846, PRC943, PRC9105, PRC1030, PRC91097, PRC946, PRC94111, PRC91153, PRC91184, PRC91187, PRC91187, PRC91187, PRC91187, PRC91187, PRC91187, PRC91188, PRC9188, PRC9188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                       Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 21; Length 249; 100.0%; Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0113686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention.
Watanabe CK, Wood WI;
                                                                                         JPI; 2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 epiddgkgl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPIDDGKGL 9
                                                                                                                                        N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200037491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ☆
```

.. O

```
may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroldism, immunological disorders, amyloldosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheiner's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                     This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87725-A8774 which encode human secreted proteins AAB87563-B25812. The proteins includes signal peptides. Included in the invention are a host cell containing one of the convention are done of the convention are done of the sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for dontifying features of the computer system, and a method for the containing features of the conversing a secreted proteins of the secreted proteins are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion overtors. The proteins of the invention
                                                                                                                                                                          Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 49; DB 21; Length 249; 100.0%; Pred. No. 0.084; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; prevention; treatment; diagnosis; disease;
                                                                             Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                       Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0141032.
99US-0469099.
99US-0141032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
'... 9; Conservē
                                                                                                                                                                                                                    mapping procedures -
                                                                                                                   WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 epiddgkgl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EPIDDGKGL 9
                                                                                                                                      N-PSDB; AAA87727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1999;
25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
RESULT
           \overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutinifiammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-mutinifiammatory; antimutagen; cardiavascular; antianaemic; anaemia; antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialergic; antiasthmatic; antidiabetic; oytostatic; immunostimulant; gene therapy; antiasthmatic; antidiabetic; oytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatological arthritis; septic shock; pancraatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer; alsabase; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                             49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 49; DB 22; Length 249; Best Local Similarity 100.0%; Pred. No. 0.084; Matches 9; Conservative 0; Mismatches 0; Indels (
Dumas Milne Edwards J, Bouqueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-457603/49.
                                                                                                         WPI; 2001-071487/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 epiddgkg| 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-FSDB; AAH99686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM25745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAM25745
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
```

```
encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic
                                                               AAH99166 to AAH99904 encode the human proteins given in AAM5225 to AAM2563. The proteins can have activities based on the tissues and cells they are expressed in, such as antiinflammatory, antirheumatic; antiarthritti; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucido; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antigerkinsonian; and immunosimulant. The proteins and polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 25752; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 22; Length 260; 100.0%; Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 25752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB66320 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL10423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB66320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB66320
```

X og

```
ó
            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more yenes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention is
                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175 and the encoded proteins
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                  .0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 29052; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                       Score 38: DB 22; Length 299;
Pred. No. 17;
1: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 29052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB67420 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                         77.68;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                 (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                       133 epvddgpg 140
                                                                                                                                                                                                                                                                                                                                           1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL11523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB67420;
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB67420
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
×888888888888888888888888
                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                         QQ
```

```
..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57377-ABR2072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 7899; 21pp + Sequence Listing; English.
                                           77.6%; Score 38; DB 22; Length 299; 75.0%; Pred. No. 17;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.6%; Score 38; DB 22; Length 2167; 85.7%; Pred. No. 1.6e+02; tive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ 1D NO 7899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD, Myers EW;
                                                                                                                                                                                                        ABB60369 standard; Protein; 2167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                           Query Match
Best Local Similarity 75.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
'-has 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2167 AA;
                                                                                                                                 133 epvddgpg 140
                                                                                                    1 EPIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL04472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        926 epvddgk 932
                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EPIDDGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001
Sequence
                                                                                                                                                                             Φ
                                                                                                                                                                                          ABB60369
                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

RESULT 11

ABG29553

```
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerledides are also used in diagnostics as expressed sequence tays for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (IS and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymelectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG03377 represent novel human manner and amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 54862; 103pp; English.
                                                                                                                                                       Novel human diagnostic protein #24494.
                                  ABG24503 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 66./۳
استوری 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS88690
                                                                                                                                                                                                                                                                                              WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                          ABG24503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                   ABG24503
RESULT
```

```
The invention relates to isolated polynucleotide (1) and probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome can gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 35; DB 22; Length 127; 66.7%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 59912; 103pp; English.
                                                                                                                           Novel human diagnostic protein #29544.
ABG29553 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                 18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||||:|:
67 eviddgrgm 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS93740.
                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                              11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                            ABG29553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                            ô
```

·,

Gaps

..

71.4%; Score 35; DB 22; Length 98; 66.7%; Pred. No. 19; 1; Indels

| ||||:|: 60 eviddgrgm 74

a

1 EPIDDGKGL 9

ò

```
antibiotic biosynthetic pathway, ORR3. A vector comprising a matibiotic biosynthetic pathway resistance gene product is useful for selecting for a transfered or transformed host cell. An integrative version of the vector is useful for introducing a everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genes micromonospora. The DNA encoding the biosynthetic proteins is useful for synthesising novel everninomicin-related compounds, arising from modifications of the DNA sequence designed to change glycosyl and modificed oresellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or other secondary metabolic products, improving the yield of everninomicin or other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of crhomycins, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterologous gene of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic resistance genes in order to carry out bioconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation processes involving e.g. Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrative vector can be used to permanently integrate copies of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence comprises one of 98 enzymes of the everninomicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 296;
                                                                                                                                                                                                           Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                             Micromonospora everninomicin biosynthetic enzyme ORF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.4%; Score 35; DB
71.4%; Pred. No. 68;
Live 2; Mismatches
                                                                                                                                                                                                                                                                                Micromonospora carbonacea var. africana
                      AAU04903 standard; Protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Fig 12; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-2000; 2000US-0175751.
                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-2001; 2001WO-US01187
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosted TJ, Horan AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442147/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                     termentation; ORF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS08699
                                                                                                                                                                                                                                                                                                                                WO200151639-A2.
                                                                                                                  26-SEP-2001
                                                                       AAU04903;
AAU04903
```

```
polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pusuliosis, hypertosis and osteomyelitis), uveritis and endophrhalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                         uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.4%; Score 35; DB 22; Length 414; ilarity 71.4%; Pred. No. 1e+02; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang SS, Bhatia A;
                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #18373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Wany .
                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 18672; 1069pp; English.
AAU57477 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000; 2000US-199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2000; 2000US-208841P. 07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L'maisonneuve J, Zhang Y,
                                                                                                                                                  13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS59583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 dpvddgk 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EPIDDGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W0200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                             AAU57477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

. 0

Gaps

. 0

0;

Conservative

Matches

δ

AAU41020 standard; Protein; 511 AA.

AAU41020

AAU41020;

```
polypeptide (II) sequences. (1) is useful as hybridisation probes, by olymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags polynucleotifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. [1] and its binding partners are useful in medical imaging of sites expressing [1]). [1] and [1]) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00101-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaqing; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 22; Length 481; 66.7%; Pred. No. 1.2e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 59914; 103pp; English.
                                                                                                                                                              Novel human diagnostic protein #29546.
                                         ABG29555 standard; Protein; 481 AA.
                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2000; 2000US-0649167.
                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                 ABG2955;
RESULT 14
                        ABG29555
```

```
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the acnes. The disorders include SAPHO Syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Practices is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or subsence of practice in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and the achieve treat P. acnes in a passocial production of antibodies and the achieve treat P. acnes in the production of antibodies and the achieve treat P. acnes in a passocial production of antibodies and the achieve treat P. acnes proteins. The antibodies can be used as an acnes in the production of antibodies and the achieve treat P. acnes and activity of P. acnes polypeptides be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                           SAPHO syndrome; synovilis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 22; Length 511; 75.0%; Pred. No. 1.3e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang SS, Bhatia A;
                                                                                   Propionibacterium acnes immunogenic protein #1916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wany -
                                                                                                                                                                                              Jermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID No 2215; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US12865.
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating acne vulgaris -
                                                                                                                                                                                                                                           Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS59513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 plddgkdl 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                    WO200181581-A2.
                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                   01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
```

ö

. 0

Conservative

qq

ô

Search completed: August 6, 2002, 16:52:54 Job time: 336 sec

Sequence 10,

US-08-476-254-10

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
Appli
Appli
Appli
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appli
                                                                     (without alignments)
4.292 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100,
                                                             August 6, 2002, 16:53:55; Search time 51.22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                         /cgnz_6/ptodata/2/laa/AB_COMB.pep:*
/cgnz_6/ptodata/2/laa/AB_COMB.pep:*
/cgnz_6/ptodata/2/laa/AB_COMB.pep:*
/cgnz_6/ptodata/2/laa/AB_COMB.pep:*
/cgnz_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgnz_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-08-470-179-14
3-08-858-207A-509
3-09-232-200-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-501-126-2
US-08-282-197C-55
US-08-687-865A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-669-974-32
-09-268-347-44
-09-396-651B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .09-136-574A-44
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-685-467-2
US-09-377-155-32
US-08-913-942-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-147-992-3
US-09-313-427-9
US-09-011-197-4
US-08-409-995-5
US-08-685-467-5
US-08-913-942-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-476-254-2
                                                                                                                                                                          231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                 US-10-020-139-2_COPY_115_123
                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                        1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match Length
                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                             Scoring table:
                                                                                                                          Sequence:
                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                           Database
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
```

```
Appli
Appli
Appli
Appli
Appli
                                       Appli
                                                                                                                                                                                                Appl
                                                                             Sequence
                                                                                                        Sequence
                                                                                                                                              Sequence S
                                                                                                                                                                                     Sequence
                                       Sequence
                                                      Seguence
                                                                   Sequence
                                                                                                                                   Seguence
                                                                                                                                                                           Seguence
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FILING DATE: 29-DEC-1995
                                                US-08-480-604A-23
US-08-405-496A-23
US-08-915-136-23
US-08-405-496A-26
US-08-915-136-26
US-08-915-294-9
US-08-145-294-9
US-08-307-2794-9
US-09-199-637A-331
US-07-779-172A-3
US-08-106-43A-2
US-08-106-43A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKALI-TOLERANT XYLANASES
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Van Solingen, Pieter
APPLICANT: Van Solingen, Pieter
APPLICANT: Williams, Diane P.
APPLICANT: Iverson, Sara
APPLICANT: Farrell, Roberta L.
APPLICANT: Farrell, Roberta L.
APPLICANT: Van Der Kleij, Wilhelmus A.
APPLICANT: Herweijer, Margaretha A.
APPLICANT: Ouax, Wilhelmus J.
APPLICANT: Ouax, Wilhelmus J.
APPLICANT: Ones, Brian E.
TITLE OF INVENTION: ALKALI-TOLERANT XYLANAS NUMBER OF SEQUENCES: 20
                                       US-09-046-086-2
                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4615-0057.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08501126
; Patent No. 6140095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 887-1500 TELEFAX: (202) 887-0763 INFORMATION FOR SED ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // MOLECULE TYPE: protein
US-08-501-126-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20006-1812
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-501-126-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
 STATE:
```

Length 396;

67.3%; Score 33; DB 4;

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jones, Kevin F.
APPLICANT: Zagursky, Robert J.
APPLICANT: Ool, Peggy
TITLE OF INVENTION: The NucA Protein of Haemophilus
TITLE OF INVENTION: influenzae and the Gene Encoding That Protein
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                             APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 33; DB 2; Length 397;
77.8%; Pred. No. 93;
Live 0; Mismatches 2; Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
      Pred. No. 93;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                             Sequence 55, Application US/08282197C; Patent No. 5871730; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/08687865A
; Patent No. 595596
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 202-371-2600
202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 397 amino acids
amino acid
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 1D NO:
                                                                                         195 EVIDDGGGL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 EVIDDGGGL 203
                                                               1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20002
                                                                                                                                                                      RESULT 2
US-08-282-197C-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-687-865A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
```

```
Sequence 2, Application US/09043711
Patent No. 6221365
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Jones, Kevin F.
APPLICANT: Zagursky, Robert J.
APPLICANT: Ooi, Peggy
TITLE OF INVENTION: The NucA Protein of Haemophilus
TITLE OF INVENTION: influencae and the Gene Encoding That Protein
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

67.3%; Score 33; DB 2; Length 603;
Best Local Similarity 85.7%; Pred: No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-NOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/687,865A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,711
                                                                                                                                        .0, Ve
.0, Ve
26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: American Cyanamid Company STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: US 08/687,865
26-JUL-1996
                                                                                                                                                                                                                                                  NAME: Gordon, Alan M. REGISTRATION NUMBER: 30,637
                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 603 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 TELECHONE: 201-50.
TELEPHONE: 201-50.
TRIPFAX: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gordon, Alan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
U.S.A.
                  U.S.A.
                                                                                                                                                                                          FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aub...
STREET: Onc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EPIDDGK 7
                                   07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U ZIP: 07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-687-865A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-043-711-2
                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            67.3%; Score 33; DB 4; Length 603; 85.7%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 65.3%; Score 32; DB 1; Length 58; Best Local Similarity 71.4%; Pred. No. 19; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Trask, Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sweigert Ph.D. Susan E. REGISTRATION NUMBER: 36,289
REGISTRATION NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPAX: 801-532-1922
TELEPAX: 801-531-9168
INPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-470-179-15
Sequence 15, Application US/08470179
Patent No. 5645994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Borrelia burgdorferi
US-08-470-179-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                               LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-043-711-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2
                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 58 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 84110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  525 EPIDDNK 531
                                                                                                                                                                                                                                                                                                             1 EPIDDGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||:|:
51 IDDGRGI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: STATE:
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                               ô
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Donovan, William P.
Donovan, Judith C.
Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
                                                                                  APPLICANT: Donovan, William P.
APPLICANT: Donovan, Judith C.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 65.3%; Score 32; DB 3; Length 267; Best Local Similarity 71.4%; Pred. No. 95; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,905 FILING DATE: Concurrently Herewith CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                  Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                       Sequence 3, Application US/08718905
Patent No. 6063756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09550497
Patent No. 6248536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-718-905-3
                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                  ADDART: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 PLDDNKG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                  COUNTRY: Un
US-08-718-905-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-550-497-3
```

```
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34 TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 32; DB 4; Length 267; 71.4%; Pred. No. 95; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%; Score 32; DB 4; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,497
FILING DATE: 14-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                             FILING DATE: <UNKNOWN)
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOHT:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 95;
                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/718,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELLAL CALLING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,905
FILLING DATE: 24-5EPE-1996
INFORMATION FOR SEO 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/147,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 267 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09147992
Patent No. 6326391
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.46
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; STRANDEDNESS: Sin
; TOPOLOGY: linear
US-09-147-992-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 PLDDNKG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PIDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-550-497-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-147-992-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
```

```
o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6171789el Insertion Sequence from a Virulent tent No. 6171789 .

TITLE OF INVENTION: Isolate of Burkholderia Cepacia, and Diagnostic and TITLE OF INVENTION: Identification Procedures Based Thereon.

NUMBER OF SEQUENCES: 16

COMPOTER READABLE FORM:

MEDIUM TYPE: Floppy disk
                                                         GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION WUMBER: US/09/323,427
CURRENT APPLICATION WUMBER: 60/087,435
EARLIRE APPLICATION WUMBER: 60/087,435
EARLIRE APPLICATION WOMBER: 60/087,435
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%; Score 32; DB 4; Length 271; 83.3%; Pred. No. 97; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 65.3%; Score 32; DB 4; Length 419; Best Local Similarity 62.5%; Pred. No. 1.5e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/002,398
FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Burkholderia cepacia
INDIVIDUAL ISOLATE: ET12/cblA
                     Sequence 9, Application US/09323427
Patent No. 6248329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-011-197-4
; Sequence 4, Application US/09011197
; Patent No. 6171789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Dirofilaria immitis
US-09-323-427-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-AUG-19
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 VDDGKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 IDDGKG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
US-09-323-427-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-011-197-4
                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

0

Gaps

0

1; Indels

1; Mismatches

231 PLDDNKG 241

qq

2 PIDDGKG 8

```
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-913-942-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%; Score 32; DB 1; Length 658; 66.7%; Pred. No. 2.5e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                  E: Flehr, Hobbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HARMOPHILUS ADHESION PROTEINS NUMBER OF SEQUENCES: GORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: Same Francisco
                                                                                                                                                                                             APPLICANT: Barenkamp, Stephen 1.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: St. Geme III, Joseph W. APPLICANT: St. Geme III, Joseph W. APPLICANT: Barenkamp, Stephen J. IITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Pred. ww.
+ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A 61053/RFT TELECOMMUNICATION INFORMATION: TELEPHONE: (415, 781-1989 TELEFAX: (415, 398-3249 TELEFAX: 910, 277299 INFORMATION FOR SEQ. ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/08/409,995
24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                    Sequence 5, Application US/08409995
Patent No. 5646259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5, Application US/08685467
; Patent No. 6060059
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.79
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 24-MAR
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 EDADEGKGL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94111-4187
                                    10 PVEPGKGL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EPIDDGKGL 9
2 PIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                 US-08-409-995-5
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-685-467-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-409-995-5
                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 3; Length 658;
Pred. No. 2.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/685,467 FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942 FILING DATE: 29-DEC-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
                                                                                                                                                                                                                                                                                                                   A-61053-2/RFT/RMS
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTOMBY AGENT INFORMATION:
              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08913942; Patent No. 6200578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A - 4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        TELEPAN: (415) 781-1999
TELEFAX: (415) 386-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                658 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RY: United States
94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-685-467-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HE NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 |:||||
350 EDADEGKGL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
```

```
ô
                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                               65.3%; Score 32; DB 4; Length 658; 66.7%; Pred. No. 2.5e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Flehr, Hobbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNBER: 38,304
REFERENCE/DOCKET NUMBER: 36,61053/RFT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMMUNICATION INFORMATION:
TELEEX: (415) 398-3249
TELEEX: (415) 398-3249
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/08/409,995
24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-409-995-2

7. Sequence 2. Application US/08409995

7. Patent No. 5646.59

6 GENERAL INFORMATION:
                   TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z1P: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              Best Local Similarity 66.79
Matches 6; Conservative
                                                                                                                                                               unknown
                                                                                                                                                                                           / MOLECULE TYPE: protein US-08-913-942-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                unknown
                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                   350 EDADEGKGL 358
                                                                                                                                                                                                                                                                                                                                                               1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-409-995-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1.4
                                                                                                                                                                                                                                                                                                                                                                                                   QQ
```

0; Gaps

Query Match 65.3%; Score 32; DB 1; Length 1098; Best Local Similarity 66.7%; Pred. No. 4.3e+02; Matches 6; Conservative 1; Mismatches 2; Indels

350 EDADEGKGL 358

g g

1 EPIDDGKGL 9

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%; Score 32; DB 3; Length 1098; 66.7%; Pred. No. 4.3e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                             APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
APLICANT: Barenkamp, HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/685,467
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-61053-2/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 6, 2002, 16:53:56
Job time: 288 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 2, Application US/08685467
Patent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) US-08-685-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
                                                                                                                                                                                                                                                                      COUNTRY: United States 21P: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Silva, Robin M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: U
                                                                                                                                                                                                        STREET: Four .....
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 EDADEGKGL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EPIDDGKGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
US-08-685-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

August 7, 2002, 06:43:38; Search time 14.84 Seconds (without alignments) 51.800 Million cell updates/sec

US-10-020-139-2_COPY_159_166 Perfect score:

1 ЕТБРОТИО 8 BLOSUM62 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

Gapup 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	5,10-methylenetetr	dissociation	GDP dissociation i	thetical profe	transori	transferase) u	methioninetRNA]	DNA polymerase III	DNA polymerase III	GDP dissociation i	hidonate 5	S	۵	+		- 54	hypothetical prote	ga-3			->	CT648 hypothetical	hypothetical prote		ε	transferrin precur	(e)	n bio	
SOFTENDED	ć	JD	AI3321		03	5	T48145	C82564	T01782	S76525	G86573	B72050	T10801	A30882	149479	T17345	BVECNP	F85982	AD1009	T08462	T10898	C98200	AF3086	G72037	B86586	T46107	H84773	in	3376	C	6904	
		108	7	7	7	CI	2	~	N	7	7	C)	7	-	7	~	-	a	7	7	N	Ο.	N	(7)	C)	N	C)	(7)	7	7	7	
	4	u a buen	274	4	マ	œ	S	\sim	444	53	4	24	4	7	^	$^{\circ}$	92	Q.	\sim	321	∞	422	2	\sim	7	436	\sim	6	0	066	CI	
uę	Query	MACCI	82.6	0	0	œ	9	9		ġ.	9	ė	m.	ω.	m	m	Ϊ.	ä	_;	71.7			÷	-			Ξ.	٦.	Ξ.	71.7	٠.	
		3001 e	38	37	37	36	35	35	35	35	35	35	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	
	Result	2	7	7	m	4	S	9	7	∞	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	

RESULT T02030

Σ

TUCOUS

GDP dissociation inhibitor protein - rice
C:Species: Oryza sativa (rice)
C:Species: Oryza sativa (rice)
C:Species: Oryza sativa (rice)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-May-2000
C:Accession: TO2030
R:Kim, C.Y.; Cheon, S.Y.; Jeong, S.Y.; Cheong, Y.H.; Choe, M.S.; Park, H.C.; Cho, I submitted to the EMBL Data Library, August 1997
A:Reference number: 214502
A:Reference number: 214502
A:Reference number: 214502
A:Residues: 1-445 <KIM>
A:Ross Treferences: EMBL:AF016896; NID:g2384757; PID:g2384758
C:Genetics:
A:Genetics:
A:Genetics:
C:Superfamily: human GDP dissociation inhibitor XAP-4

hypothetical prote		traE protein homol	hypothetical prote	probable DNA-bindi	myb-related protei	myb-related protei	myb-related protei	myb-related protei	hypothetical prote	asparaginetRNA 1	hypothetical prote	choline dehydrogen	probable atsF prot		S
097991	F75400	T31239	T08326	D85096	T02984	868688	JQ0957	T09879	T19149	E70112	S75491	AC0143	F70651	C43674	S15727
:1	?	~	7	7	?	_	٦	2	C)	~	C)	C)	:\	~	7
109	146	207	233	236	239	249	274	294	416	466	522	267	603	669	739
9.69	9.69	9.69	9.69	9.69	9.69	69.6	69.6	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69
~1	3.2	32	32	3.2	32	32	3.2	35	32	3.5	3.2	32	32	32	32
e															

ALIGNMENTS

RESULT 1
5.10-methylenetetrahydrofolate reductase (EC 1.7.99.5) [imported] - Brucella meliter C.Species: Brucella melitensis
C:Date: 01-Feb-2002 #Sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C:Accession: A13321
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivance, Mazur, M.; Goltsman, E.; Selkov, E.; Rizer, P. H.; Hanjus, S.; O'Callanhan, D. 11.
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella mel: A;Reference number: AD3252; PMID:11756688
A:Accession: A1321 A:Status: proliminary
A; Molecule type: DNA
A;Residues: 1-274 <kur></kur>
A.Cross references: GB.BE008917; PIDN:AAL51740.1; PID:917982477; GSPDB:GN00190
C.Genetics:
A;Gene: BME10559
A; Map position: I
C.kuperiamily: 5,10-methylenetetranydrofolate reductase (FADH2) C.Keywords: oxidoreductase
Query Match 82.68; Score 38; DB 2; Length 274; Best Local Similarity 75.08; Brad NO 6.0.
ative
QY 1 ETUPQTHQ 8

```
Cargedies: Xylella fastidiosa
Cispecies: Xylella fastidiosa
Cispecies: Xylella fastidiosa
Cispecies: Xylella fastidiosa
Cispecies: Aylella fastidiosa
Cisteesidon: C8264
Riandorymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Se Riandorymous: The Xylella fastidiosa.

Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome sequence of the plant pathogen Xylella fastidiosa.
Aitle: The genome Xilella fastidiosa.
Aitle
                          R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                A;Wolecule Lype: DNA
A;Residues: 1-250 <HBV>
A;Tessidues: 1-250 <HBV>
A;Experimental source: cultivar Columbia; BAC clone T4C9
C;Genetics:
A;Map position: 4
A:Nutrons: 22/2; 52/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 35; DB 75.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDP dissociation inhibitor - common tobacco C; Species: Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: aspartate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 85.7
                                                                                                                           A;Reference number: 224485
A;Accession: T48145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | || || |||
| 84 EIDPSTHQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ЕТВРОТНО 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 TEPYTHO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: XF2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
C82564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotherical protein F16A16.130 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04523
C:Accession: T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Oryza sativa (rice)
C;Decies: Oryza sativa (rice)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-May-2000
C;Dacession: T02032
R;Kim, C.Y.; Cheon, S.Y.; Jeong, S.Y.; Cheong, Y.H.; Choe, M.S.; Park, H.C.; Cho, M.J.
Submitted to the EWBL Data Library, August 1997
A;Reference number: X14502
A;Residues: 1-445 < KIM>A;Residues: 1-445 < KIMA
A;Residues: 1-445 < KIMA
A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transcription factor - Arabidopsis thaliana NATternate names: protein T4C9.190 C;Species. Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession:\text_t4148145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
     80.4%; Score 37; DB 2; Length 445; 75.0%; Pred. No. 18; 1: Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.4%; Score 37; DB 2; Length 445; 75.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.3%; Score 36; DB 2; Length 880;
87.5%; Pred. No. 59;
                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDP dissociation inhibitor protein - rice
Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                      151 EADPKTHQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 EADPKTHO 158
                                                                                                                                                                                                           1 ETDPOTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ETDPOTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 ETLPOTHQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
DNA polymerase III, alpha chain CP0081 [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change II-May-2000
C;Accession: B72050; E81616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain CWL029
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hici, C.; Dodson, R.; Gwinn, W.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzl Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR A; Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 1-1240 (REA>
A.Cross-references: GB:AE002171; GB:AE002161; NID:97189009; PIDN:AAF37967.1; PID:g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood
Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1-1240 <ARN>
A.Cross-references: GB:AF001649; GB:AE001363; NID:g4376963; PIDN:AAD18805.1; PID:g4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Beyser, K.; Fabry, S. submitted to the EMBL Data Library, July 1996
A.Description: Identification and characterization of a lower plant Ypt/Rab guanosi
A.Reference number: 217156
A.Recession: T10801
A.Status: preliminary, translated from GB/EMBL/DDBJ
                    A;Cross-references: GB:BA0000008; NID:g8979038; PIDN:BAA98873.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Volvox carteri f. nagariensis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: B72050
                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%: Score 35; DB 2; Length 1240; 75.0%; Pred. No. 1.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                 Score 35; DB 2; Length 1240;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDP dissociation inhibitor GDI1 · Volvox carteri f. nagariensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-443 - EBEX>
A;Cross-references: EMBL:U62866; NID:91572517; PID:91572518
A;Experimental source: strain HK10
                                                                                                                                                     C;Superfamily: DNA-directed DNA polymerase Ill alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: dnaE; CP0081
C;Superfamily: DNA-directed DNA polymerase III alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                     76.1%;
75.0%;
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.08
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         525 ETOPDLHQ 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 ETDPDLHQ 532
                                                                                                                                                                                                                                                                                                                                                                               1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: E81616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T10801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                       A;Gene: dnaE
                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <KAN>
A;Residues: 1-532 <KAN>
A;Cres-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10371.1; PID:g100164
A;Cres: the nucleotide sequence was submitted to the EMBI. Data Library, June 1996
C;Superfamily: methionine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rishirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
ArTitle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase III alpha [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr.1997 #sequence_revision 25-Apr.1997 #text_change 20-Jun-2000
C:Accession: S76525
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 26-May-2000
C;Accession: T01782
R;Ezaki, B.; Koyanaqi, M.; Gardner, R.C.: Marsumoto u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methionine--tRNA ligase (EC 6.1.1.10) · Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDI
C;Function:
A;Description: inhibits dissociation of GDP from GTP binding proteins
C;Superfamily: human GDP dissociation inhibitor XAP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 35; DB 2; Length 444; 62.5%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 532;
                                        Ricasti, B.; Koyanagi, M.; Gardner, R.C.; Matsumoto, H. submitted to the EMBL Data Library, July 1997
A:Reference number: Z14424
A:Accession: T01782
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Relates: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-444
A:Residues: 1-444
A:Residues: EMBL.AF012823; NID:g2501849; PID:g2501850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.1%; Score 35; DB: 85.7%; Pred. No. 53; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                                                                                          Experimental source: cultivar Samsun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85,7,2
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1240 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 ESDPKTHE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ELDPOTH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S76525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: G86573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

```
Search completed: August 7, 2002, 06:44:03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
,
                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-1223 <DUE>
A,Cross-references: EMBL:AL117665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 75.00
The following the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||:| |
1040 ETDPETSQ 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JV0027
A; Molecule type: DNA
A; Residues: 1-92 <CHO>
                                                                                                                                                                                                            A, Accession: T17345
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DPQTHE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Job time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Balcarek, J.M.; Theisen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, B. Bol. Chem. 263, 13937-13941, 1988
A; Title: Isolation and characterization of a cDNA clone encoding rat 5-lipoxygenase. A; Reference number: A30882; MUID:88330933
A; Accession: A30882
A; Molecule type: MRNA
A; Residues: 1-670 «BAL»
                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A30882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arachidonate 5-lipoxygenase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-jul-1996 #sequence_revision 02-jul-1996 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J03960; NID:9205228; PIDN:AAA41538.1; PID:9205229 C;Superfamily: arachidonate 5-lipoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross-references: GB:L42198; NID:g886332; PIDN:AAC37673.1; PID:g886333 C;Genetics: A)Gene: Alox5 C;Superfamily: arachidonate 5-lipoxygenase
A;Description: Inhibits dissociation of GDP from GTP binding proteins C;Superfamily; human GDP dissociation inhibitor XAP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.9%; Score 34; DB 1; Length 670; Best Local Similarity 75.0%; Pred. No. 1.1e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 674;
                                                                                                                                                                 73.9%; Score 34; DB 2; Length 443; 62.5%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.9%; Score 34; DB 2; Length 674
75.0%; Pred. No. 1.1e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKF2p586M1824.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arachidonate 5-lipoxygenase (EC 1.13.11.34) - rat
                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                 Query Match
Best Local Similarity 62...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-674 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                           151 ESDPKTHK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 KTDPCTHQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 KTDPCTHQ 304
                                                                                                                                                                                                                                                                                                                             1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
A.Cross-references: GB:x68873; NID:942128; PIDN:CAA48736.1; PID:942129
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1433-1462, 1997
A:Title: The complete genome sequence of Escherichia (Ji K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AF000399; GB:U00096; NID:g2367201; PIDN:AAC76220.1; PID:g178<sup>c</sup> A;Experimental source: strain K-12, substrain MG1655 C;Comment: This protein is involved in positive regulation of the metabolism of suga C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Choi, Y.L.; Nishida, T.; Kawamukai, M.; Utsumi, R.; Sakai, H.; Komano, T. J. Bacteriol, 171, $722-5255, 1989
A;Title: Cloning and sequencing of an Escherichia coli gene, nlp, highly homologous A;Reference number: JV0027; MJID:89359178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar fermentation stimulation protein B (NER-like protein) - Escherichia coli N.Alternate names: ner-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Reference number: A64720; MUID:97426617
A:Accession: F65109
A:Status: preliminary: nucleic acid sequence not shown; translation not shown A:Rolecule type: DNA
A:Rolecule type: DNA
A:Residues: 1-92 <BLAT>
C,Species: Homo sapiens (man)
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C,Accession: T17345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 27-Nov-2001
C;Accession: JV0027; F65109
                                                                                                            R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: 218727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.7%; Score 33; DB 1; Length 92; Best Local Similarity 83.3%; Pred. No. 20; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 A,Experimental source: adult uterus; clone DKF2p586M1824 C,Genetics:
A;Note: DKF2p586M1824.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: nlp
A.Map position: 69 min
G.Superfamily: phage D108 DNA-binding protein
C.Keywords: DNA binding; transcription regulation
F:50-68/Region: DNA binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
```

```
homo sapien
meiothermus
borrelia bu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       emericella
herpes simp
clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemophilus
bacillus sp
bacillus oh
                                                                                                                                                                                                                                                                                                                                                       chlamydia p
homo sapien
mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sus scrofa
camelus dro
                                                                                                                                                                                                                                                                                                                                                                                                                   deinococcus
equus cabal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dictyosteli
arabidopsis
                                                   August 7, 2002, 06:44:08; Search time 10.33 Seconds (without alignments) 29:986 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             Q55729 synechocyst
                                                                                                                                                                                                                                                                                                                                                                                  rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                            phaseolus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                            096db9
P51399
P12527
P48999
P18837
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9rx13
P27425
O94833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P27036
                                                                                                                                                                                                                                                                                                                                                         09z7n8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        029545
GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                  105224 seqs, 38719550 residues
                                                                                      US-10-020-139-2_COPY_159_166
                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRPA_SYNPY
LEC_SOYBN
KSGD_ARATH
INTA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIRE_HUMAN
YTFM_HAEIN
CDGT_BACS2
CDGT_BACOH
                                                                                                                                                                                                                                                                                                                                                       DP3A_CHLPN
FXY5_HUMAN
LOX5_MESAU
LOX5_RAT
LOX5_MOUSE
SFSB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYN_BORBU
TAC3_MOUSE
SCOB_EMENI
VGLG_HSV2H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUNF_CLOTM
TAC3_HUMAN
HBP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   MURE_DEIRA
TRFE_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRTC_DICDI
KSGT_ARATH
                                                                                                                                                                                                                                Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACFX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROB_MEIRU
                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                            FD3E_PHAAU
                                                                                                                                                                                                                                                                                                                                              SYM_SYNY3
                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                        Maximum Match 100%
                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                              Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                 SwissProt_40:*
                                                                                                46
1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                              Score
                                                                                                  Perfect score:
                                                                                                                                                                                                                                                   Database :
                                                                                                         Sequence:
                                                                                                                                                     Searched:
                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                          Title:
```

aquifex aeo

eguus cabal

09tum0

TRFL_CAMDR DNLJ_AQUAE

P08238 homo sapien P11499 mus musculu O57521 brachydanio Q04619 gallus gall Q99474 brachydanio P11501 gallus gall P07900 homo sapien P46633 cricetulus P07901 mus musculu O02705 sus scrofa Q99563 homo sapien Q59119 aeromonas h	RESULT STR. STANDARD: PRT: 532 AA. D. SYNYANY STANDARD: PRT: 532 AA. D. SYNYANY STANDARD: PRT: 532 AA. D. SYNYANY D. SYNYANY STANDARD: Last sequence update) D. NOV-1997 (Rel. 35, Created) D. NOV-1997 (Rel. 35, Last sequence update) D. NOV-1997 (Rel. 35, Last sequence update) D. SYNCHOCYSTIS STRONDARD: BLAST SCHOOL Update) D. SYNCHOCYSTIS STRONDARD: BCC 6.1.1.10) (Methionine
1 HS9B_HUMAN 1 HS9B_MOUSE 1 HS9B_BRARE 1 HS9B_CHICK 1 HS9A_CHICK 1 HS9A_CHICK 1 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 2 HS9A_CHIGR 4 HS9A_CHIGR 6 HS9A_CHIGR 7 HS9A_CHIGR 7 HS9A_CHIGR 8 HS9A_CHIGR 1 CDBG_HUMAN	ALIGNMENTS SYNY3 STANDARD: PRT; 532 AA. 29; 29; 20; 20; 20; 20; 20; 20;
67.4 723 67.4 725 67.4 725 67.4 725 67.4 726 67.4 732 67.4 732 67.4 732 67.4 732	SYNY3 SYNY3 SYNY3 SYN_SYNY3 SYN_SYNY3 STANDARD; PR7 01-NOV-1997 (Rel. 35, Last sequer 16-007-2001 (Rel. 40, Last annote Methionyl-tRNA synthetase (EC 6.1 Methonyl-tRNA synthetase (EC 6.1 Synechocystis sp. (strain PCC 680 NCB1-TaxID-1148; SEQUENCE FROM N.A. MEDLINE-96127529; PubMed-8590279, Kaneko T., Tanaka A., Sato S., K Sugiura M., Tabata S.; Sequence analysis of the genome Synechocystis sp. strain PCC6803 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 FROUTRED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1 TRNAFMED NOT ONLY FOR ELDONA FOR THE INITIATION OF ALL MR1
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	SYM_SNNY3 SYN_SNNY3 ID SYN_SNNY3 SYN_SNNY3 ID 01-NOV-1997 (Rep) DT 01-NOV-1997 (Rep) DT 01-NOV-1997 (Rep) DT 01-NOV-1997 (Rep) DE Methionyl-tRNA synchronyl-tRNA synchronyl-tr
	R R R R R R R R R R R R R R R R R R R

EMBL; AE001649; AAD18805.1; -. EMBL; AE002171; AAF37967.1; -. EMBL; AP002547; BAA98873.1; -.

CP0081

TIGE;

```
..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the PMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelab.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 28:2317-2314 (2000).

-I-FUNCTION: DNA POLYMERASE 111 IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.

THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.

THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).

-I-CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Chinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Shii K., Hattori M., Kullara S., Nakazawa T.; "Comparison of whole grenome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gwinn M., Metaow ...
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
nnoumnniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND CHI, AND WITH THE BETA CHAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPISSMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
76.1%; Score 35; DB 1; Length 532; 85.7%; Pred. No. 16; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila,
                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae (Chlamydophila pneumoniae)
                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
bus polymerase 111 alpha subunit (EC 2.7.7.7).
                                                                                                                                                                                                                                   PRT; 1240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99206606; PubMed~10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20330349; PubMed-10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20150255; PubMed-10684935;
                    Best Local Similarity 85,79
Matches 6; Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID~83558;
                                                                                                                         68 ELDPOTH 74
                                                                                 1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + [DNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY
                                                                                                                                                                                                                                 DP3A_CHLPN
Q927N8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-AR39
  Query Match
                                                                                                                                                                                                               DP3A_CHLPN
                                                                                     δ
                                                                                                                            q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen S.-J., Chen S.-J., Chen S.-J., Chen S.-J., Chen S.-J., Shon Y., Wu G.-M., Chen S.-J., Chen S.-J., Shon Y.-Y., Shong J.-W., Shon S.-J., Chen S.-J., Chen S.-J., Chen S.-J., Shon Youndelined genes expressed in CD34+ hematopoietic Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FXY5_HUMAN STANDARD; PRT; 178 AA.
096089; Q9P039; Q9HC34;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 5 precursor (HSPC113).
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                 76.1%; Score 35; DB 1; Length 1240; 75.0%; Pred. No. 40; Live 0; Mismatches 2; Indels
                                                                                                                                             SMART: SM00481, POLITIAC, 1.
Transferase: DNA-directed DNA polymerase: DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBL_TaxID=9606;
                                                                                                                                                                                                 1240 AA; 140074 MW; 7D6890EF002A88E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Blood;
MEDLINE-20499367; PubMed-11042152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF161462; AAF29077.1; -.
                                                                              InterPro; IPR004013; PHP_C.
InterPro; IPR003141; PHP_N.
                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 75.09
Matches 6; Conservative
                                                                                                             Pfam; PF02811; PHP_C;
Pfam; PF02231; PHP_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                  Complete proteome.
SECUENCE 1240 AA
                                                                                                                                                                                                                                                                                                                                                   525 ETDPDLHQ 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                   1 ЕГОРОТНО В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FXYD5 OR IWU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                   FXY5_HUMAN
δ
```

```
InterPro; IPR001024; LH2
                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labs.ib.ch).
                                                                                                                                                                                                                                          0
                                                                                                                          MSPSGRLCLLTIVGLILPTRGQŤLKDTTSSSSADSTIMDIQ
VPTRAPDAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTD
GPLVTDPETHKSTKA -> MQTLSNIPCFCLHGSLLPSTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitzler J.W., Eling T.E.; "Cloning, sequencing and expression of a 5-lipoxygenase from Syrian
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                             FXYD DOMAIN-CONTAINING ION TRANSPORT
                                                                                                                                                                                                                                         :0
                                                                                                                                                                                                                     73.9%; Score 34; DB 1; Length 178; 71.4%; Pred. No. 7.6;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                      ATLS (IN ISOFORM 2).
S -> A (IN DBSNP:1688005).
                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                 HT -> SH (IN REF. 1)
7429D5A838B75AA1 CRC64;
                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 EM<sup>B</sup>L; BC009642; AAH09642.1; -.
EMBL; AF177940; AAG09301.1; -.
InterPro; IPR00272; ATPIG1_PLM_MAT8.
Effan; PF02038; ATPIG1_PLM_MAT8.1,
PROSITE: PS01310; FXYD; 1.
Transmembrane; Signal; lonic channel; Ion transport;
                                                                                                                                                                          /FTId~VAR_012349.
                                                                                                                                                                                                                                         2; Mismatches
                                                                                       REGULATOR 5
                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                    Alternative splicing; Polymorphism. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97109716; PubMed=8951996;
                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                            19453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U4333; AAA85257.1; -. HSSP; P12530; 1LOX.
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                            178
                                                                                               145
164
178
97
                                                                                                                                                               35
                                                                                                                                                                                   141
                                                                                                                                                                                            178 AA;
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10036;
                                                                                               22
146
165
                                                                                                                                                                35
                                                                                                                                                                                   140
                                                                              22
                                                                                                                                                                                                                                                                              87 TDPETHK 93
                                                                                                                                                                                                                                                             2 TDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SYRIAN;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus
                                                                                                                                                                                                                                                                                                                           LOX5_MESAU
P51399;
                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                          Query Match
                                                                                                         TRANSMEM
                                                                                                                             VARSPLIC
                                                                                                                                                                 VARIANT
                                                                                                DOMAIN
                                                                                                                   DOMAIN
                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                    LOX5_MESAU
                                                                                                                                                                                                                                         Matches
     ò
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ARACHIDONATE + O(2) = (6E,82,112,142)-(5S)-5-HYDROPEROXYCOSA-6,8,11,14-TETRAENOATE (THE PRODUCT IS RAPIDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88330933; Pubmed-3417684;
Balcarek J.M., Theisen T.W., Cook M.N., Varrichio A., Hwany S.-M.,
Strohsacker M.W., Crooke S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS OF LEUKOTRIENES.

-- SUBCELLULAR LOCATION: CYCOPlasmic.

-- SIMILARITY: BELONGS TO THE LIPOXYGRNASE FAMILY.

-- CAUTION: REF. 2 SUGGESTS THAT THIS PROTEIN HAS A DIFFERENT C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minor W., Steczko J., Bolin J.T., Otwinowski z., Axelrod B.; "Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1."; Blochemistry 32:6320-6323(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Isolation and characterization of a cDNA clone encoding rat 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                              Oxidoreductase; Dioxygenase; Iron; Leukotriene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 672; Pred. No. 32; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       1F7234B5C297B30F CRC64;
                                                                                                                                                                                                                                                                         IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672 AA.
                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 263:13937-13941(1988).
                                                                                                                                    PROSITE; PS00081; LIPOXYGENASE_2; 1. PROSITE; PS00711; LIPOXYGENASE_1; 1.
     IPR000907; Lipoxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93298753; PubMed-8518276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: REF.2 SUGGESTS THAT
TERMINUS DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONVERTED TO LEUKOTRIENE A4)
                       Pfam: PF00305; lipoxygenase; l. pfam: PF01477; PLAT; l.
                                                                                PRINTS; PRO0087; LIPOXYGENASE.
SMART; SM00308; LH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                    77741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.98;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                            366
371
549
672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 666-669.
                                                                                                                                                                                                                                                                                                                          549
672
672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 KTUPCTHQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoxygenase.";
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOX5_RAT
                                                                                                                                                                                                                                                     INIT_MET
                                                                                                                                                                                                                              Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P12527
                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1.0X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

; 0

```
q
                                                                                                                                                                                                                                                                                                                                                    ò
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BRBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or Weend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and gene chromosomal assignment of mouse 5-lipoxygenase.";
J. Balol. Chem. 270:17993-17999(1995)
-i- CATALYTIC ACTIVITY: ARCHLDOMATE + 0(2) ~ (6E.82,112,142)-(5S)-5-
HYDROPEROXYCOSA-6,8,11,14-TETRAENOATE (THE PRODUCT IS RAPIDLY
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA cloning, expression, mutagenesis, intracellular localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa: Chordata: Craniata, Vortebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -S., Naumann T.A., Kurre U., Jenkins N.A., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONVERTED TO LEUKOTRIENE A4).
-!- COFACTOR: IRON, ALSO REQUIRES CALCIUM AND ATP FOR ACTIVITY.
-!- PATHWAY: THIS ENZYME CATALYSES THE FIRST TWO STEPS IN THE
                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                       PROSITE: PS00081: LIPOXYGENASE_2: 1.
PROSITE: PS00081: LIPOXYGENASE_1: 1.
Oxidoreductase: Dioxygenase: Iron: Leukotriene biosynthesis:
Calcium.
INIT_MET 0 0
                                                                                                                                                                                                                          IRON (BY SIMILARITY).
IRONSVAI -> FOTV (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                               73.9%; Score 34; DB 1; Length 672; 75.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS OF LEUKOTRIENES.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6 X 129/SV; TISSUE-Peritoneal cavity; MEDLINE=95355399; PubMed+7629107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 AA.
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                       Interpro; IPR001024; LH2.
Interpro; IPR000907; Lipoxygenase.
                                                                                    Pfam; PF00305; lipoxygenase; 1.
Pfam; PF01477; PLAT; 1.
                                                                                                                   PRINTS; PR00087; LIPOXYGENASE. SMART; SMO0308; LH2; 1.
                                                                                                                                                                                                                                                                                                   77956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L42198; AAC37673.1; .. HSSP; P12530; 1LOX.
             EMBL; J03960; AAA41538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                Conscrvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                          366
371
549
672
672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                             PIR; A30882; A30882.
                                                                                                                                                                                                                                                                                    666
672 AA;
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conscrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       295 KTDPCTHQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                           1 ETDPOTHQ 8
                                          P12530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOX5_MOUSE
                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X.
                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOX5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         a
ô
```

```
MEDLINE-89359178; PubMed-2670911; Choi Y.-L., Nishida T., Kawamukai M., Utsumi R., Sakai H., Komano T.; "Cloning and asquencing of an Escherichia coli gene, nlp, highly homologous to the ner genes of bacteriophages Mu and D108."; J. Bacteriol, 171:5222-5225(1989).
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-KI2 / MG1655.
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Pluukett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Butland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anartharama T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                       SMART; SM00308; LH2; 1. POXYGENASE_2; 1. PROSTER; PS00081; LIPOXXGENASE_1; 1. PROSTUE; PS00711; LIPOXXGENASE_1; 1. Oxidoreductase; Dioxygenase; Iron; Leukotriene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sugar fermentation stimulation protein B (Mer-1ike protein).
SFSB OR NLP OR SFS7 OR B3188 OR 24551 OR ECS4067.
                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 673;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                    IRON (BY SIMILARITY).
0B2910477A3B7085 CRC64;
                                                                                                                                                                                                                 IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AA
                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                BY SIMILARITY
MGD; MGI:87999; Alox5.
InterPro; IPR001024; LH2.
InterPro; IPR000907; Lipoxygenase.
                                                                                                                                                                                                                                                     IRON
                                                                                                                                                                                                                                    IRON
                                                    Pfam; PF00305; lipoxygenase; l. Pfam; PF01477; PLAT; l.
                                                                                        PRINTS; PR00087; LIPOXYGENASE.
                                                                                                                                                                                                                                                                                     77868 MW;
                                                                                                                                                                                                                                                                                                                                         73.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                              367
372
372
550
673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax1D=562, 83334;
                                                                                                                                                                                                               367
372
372
550
673
673 AA;
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               296 KTDPCTHQ 303
                                                                                                                                                                                                                                                                                                                                                                                                             1 ETDPOTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFSB_ECOL1
P18837;
                                                                                                                                                                                                INIT_MET
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                 Calcium
                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                       METAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFSB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                          Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto K.T., Mori H., Imaseki H.;
"Novel mRNA sequences induced by indole-3-acetic acid in sections of
"Novel mRNA sequences induced by indole-3-acetic acid in sections of
elongating hypocotyls of mung bean (Vigna radiata).";
Plant Cell Physiol. 33:13-20(1992).
-!- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
SiRAIN=0157:H7 / RIMD 0509952;

MEDLLINE=21156231; Pubmed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                    O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
- i. FUNCTION: THIS PROTEIN IS INVOLVED IN POSITIVE REGULATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; DNA-binding; Activator; Complete proteome. Mon So 69 H-T-H MOTF (BY SIMILARITY).

CONFLICT 74 74 74 74 79 (IN REF. 4).

SEQUENCE 92 AA3: 10495 MW: 4B3859604F4259EC (RC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0T-1993 (Rel. 27, Last sequence update)
01-0R-2002 (Rel. 41, Last annotation update)
0mega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
(Indole-3-acetic acid induced protein ARG1).
                                                                                                                                                                                                                                        BELONGS TO THE NER FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 33; DB 1; Length 92;
83.3%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phaseolus aureus (Mung bean) (Vigna radiata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000399; AAC76220.1; ...
EMBL; AE005547; AAC58322.1; ...
EMBL; AP002564; BAB37490.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X68873; CAA48736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U18997; AAA57989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                               METABOLISM OF SUGARS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG10656; nlp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JV0027; BVECNP.
HSSP; P06020; 1NEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOLIPIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hypocotyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3916;
                                                                                                                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 DPQTHE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FD3E_PHAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FD3E_PHAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphlle W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last sequence update)
UDP-N-acctylmuramoylalaryl-p-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13) (UDP-N-acctylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase).
           -:- SUBCELLULAR LOCATION: Endoplasmic reticulum.
-:- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
-:- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
--- NDV/ OR BE INVOLVED IN METAL ION BINDING.
--- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 33; DB 1; Length 380; 62.5%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1C005117A8DAE16B CRC64;
-! - PATHWAY: PULYUNSATURATED FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                           HISTIDINE BOX 1. HISTIDINE BOX 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HISTIDINE BOX 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                          IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                     Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                43996 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 286:1571-1577(1999)
                                                                                                                                                                                                                                                          EMBI.: D14410; BAA03306.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diaminoheptanedioate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                           78
231
256
101
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 QTDPKLHQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           radiodurans Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURE OR DR0297
                                                                                                                                                                                                                                                                                                                                             Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MURE_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=R1
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9RXL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MURE_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSUB-EXTREMENTYONIC LISSUE;
MCDOWell K.J., Adams M.H., Baker C.B.;
MCDOWell K.J., Adams M.H., Baker C.B.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE ITEN BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE
TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION
TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO
HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eguus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissolactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Serotransferrin precursor (Siderophilin) (Beta-1-metal binding
                                                                                                                                                                                                                                                                                                                               Pfam: PF01225; Mur_ligase; 1.
Pfam: PF02875; Mur_ligase_C: 1.
Peptidoglycan synthesis; Cell wall; Cell division: Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%; Score 33; DB 1; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             113 119 ATP (POTENTIAL).
490 AA; 52316 MW; 46C748E9768754CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- TISSUE SPECIFICITY: PLASMA.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i' SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 706 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 36; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carpenter M.A., Broad T.E.;
"The cDNA sequence of horse transferrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1173:230-232(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBUNIT: MONOMER.
-:- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                         Interpro; IPR000713; Mur_ligase.
Interpro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93277958; PubMed-8504171;
                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Complete proteome.
                                                                                                                                                                                                                                   EMBL; AE001890; AAF09877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                          HSSP; P11880; 1GG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ETDPOT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ETDPQT 6
                                                                                                                                                                                                                                                                               TIGR; DR0297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRFE_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   globulin).
                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRFE_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
1A0FA566C0409D8A CRC64;
                                                                                                                                                                                      Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
SIGNAL 1981 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                        . . . . . . . . . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANION (POTENTIAL).
ANION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                            SEROTRANSFERKIN.
                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1065 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00205; TRANSFERRIN_1; 2. PROSITE: PS00206; TRANSFERRIN_2; 2. PROSITE; PS00207; TRANSFERRIN_3; 2.
                                                                                                      InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin: 2
                                                                                                                       Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.78;
71.48;
                                                                   EMBL; M69020; AAA30958.1; -.
                                                                             AAA63684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trabeculin-beta (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                    PIR; S33761; S33761.
HSSP; P02787: TARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515
706 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :1:11||
104 KTEPQTH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACFX_HUMAN
094833;
                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIAA0728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACFX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                    Nagase T., Ishikuwa K.-f., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Eukaryota, Metazoa; Chordala; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Calarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus/Deinococcus group; Thermus group; Meiothermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rcl. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK).
                                                                                                                                                                         DNA Res. 5:277-286(1998).
-!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
-!- SIMILARITY: CONTAINS 7 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1; Length 1065;
Pred. No. 84;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )3 EF-HAND 1 (POTENTIAL),
19 EF-HAND 2 (POTENTIAL),
121325 MW: 1701547C12D4249E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00243; GAS2; 1.
SMART; SM00243; GAS2; 1.
SMART; SM00150; SPEC; 5.
PROSTTE; PS00018; EF HAND; 2.
ACLIN-binding; Cytoskeleton; Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 6.
SPECTRIN 6.
                                                                                     MEDLINE=99087487; PubMed-9872452;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR003108; GAS2.
InterPro: IPR002017; Spectrin.
Pfam: PF00035; efhand; 2.
Pfam: PF02187; GAS2; 1.
                                                                                                                                                                                                                                                                                                                                                          EMBL; AB018271; BAA34448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pram; PF02187; GAS2; 1.
Pfam; PF00435; spectrin; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 75.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186
300
404
522
522
626
692
728
1065 AA;
                                                                                                                                                                                                                                                                                                                                                                        P02631; 10MD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || || || 1
| 1023 ETVPQTHR 1030
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meiothermus ruber.
                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermu
NCBI_TaxID=277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROB_MEIRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA_BIND
CA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
PROB_MEIRU
 qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           Neumivakin L.V.;
Neumivakin L.V.;
Neumivakin L.V.;
"Molecular clouding and sequence analysis of the proA gene from
"Molecular clouding and sequence analysis of the proA gene from
thermophilic cubacturium Thermus rubcr. The thermophilic cubacturium Thermus rubcr. The Submitted (WVV-1998) to the EMBL/Genhank/DbBJ databases.
-!- FINCTION: Catalyzes the transfer of a phosphate group to glutamate
to form glutamate 5-phosphate which rapidly cyclizes to 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigara R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Pougherty B., Tomb J. F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Vutt. R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)
                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                   Yaklichkin S.Y., Zimina M.S., Yurchenko Y.V., Hromov I.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%; Score 32; DB 1; Length 377; 71.4%; Pred. No. 43;
                                                                                                                                                                                                               -:- PATHWAY: Proline biosynthesis pathway; first step. -:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -:- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              >>. Venter J.C.;
sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Kinase; Proline biosynthesis.
SEQUENCE 377 AA; 40591 MW; F637DFE9DD811155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spirochaetales; Spirochaetaceae; Borrelia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00902; GLUTAMATE_5_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF082661; AAC72812.1; ALT_INIT.
InterPro; IPR001049; Aakinase.
InterPro; IPR001057; Glut_5_kinase.
InterPro; IPR002478; PUA.
Pfam; PF00696; aakinase; 1.
Pfam; PF01472; PUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0474; GLUSKINASE.
SMART; SM00359; PUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.48
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EADPRTH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ETDPOTH 7
                                                                                                                                                                                                  phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASNS OR BB0101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYN_BORBU
051128;
STRAIN-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AsnRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYN_BORBU
δ
```

```
a
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the PMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulres a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó:
                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + L-asparagine + LRNA(Asn) = AMP + diphosphate + L-asparaginyl - LRNA(Asn).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1042; TRNASYNTHASP.
PROSTIE; PS00179; AA_TRNA_LIGASE_II_1; 1.
PROSTIE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sadek C.M., Jalaguier S., Feeney E.P., Aitola M., Damdimopoulos A.E., Pelto-Huikko M., Gustafsson J.A.; "Isolation and characterization of AINT: a novel ARNT interacting protein expressed during murine embryonic development."; Mech. Dev. 97:13-26(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99296831; PubMed=10366448; Still I.H., Vince P., Cowell J.K.; "The third member of the transforming acidic coiled coil-containing gene family, TACC3, maps in 4p16, close to translocation breakpoints lim multiple myeloma, and is upregulated in various cancer cell lidss.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CELL GROWTH AND DIFFERENCIATION. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAC3_MOUSE STANDARD; PRT; 631 AA.
09JJ11; 09WVK9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transforming acidic coiled-coil containing protein 3 (ARNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.6%; Score 32; DB 1; Length 466; 71.4%; Pred. No. 54; U. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      466 AA; 53600 MW; 2B5900C0E6DBD1F6 CRC64;
                                                                                                                                                                                                                                                                  InterPro, IPR002106; AA_tKNA_ligase_1f.
InterPro, IPR002309; tkNA-synt_2.
InterPro, IPR002312; tkNA-synt_asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-NIH Swiss; TISSUE-Embryo;
MEDLINE-20480355; Pubmed-11025203;
                                                                                                                                                                                                                     EMBL; AE001123; AAC66501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                               Pfam; PF00152; tRNA-synt_2;
Pfam; PF01336; tRNA_anti; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 58:165-170(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interacting protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                    Q52428; 1B8A.
                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 ETDPETY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACC3 OR AINT
                                                                                                                                                                                                                                                    BB0101;
                                                                                                                                                                                                                                                      TIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
   ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement, is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHODUCED BY ALTERNATIVE SPLICING.
-:-TISSUE SPECIFICITY: EMERYONICALLY EXPRESSED.
-:-TISSUE SPECIFICITY: EMERYONICALLY EXPRESSED.
-:-DEVELOPMENTAL STAGE: AT 9 DAYS POSTCOITUM (PC), THE EXPRESSION IS STRONG IN THE NEUROEPITHELLUM.

STRONG IN THE NEUROEPITHELLUM OF NEURAL TUBE AND IN PLACENTA. AT 13 DAYS PC, THE EXPRESSION IS SEEN IN LUNG, KIDNEY, INTESTINES, THE STRONG EXPRESSION IS SEEN IN LUNG, KIDNEY, INTESTINES, THE ORDERATE SIGNAL IS DETECTED IN THE CARTILAGE PRIMORDIUM OF DEVELOPING RIBS, TOOTH AND EYE. BY 17 DAYS PC, THE TISSUE DISTRIBUTION CHANGES SO THAT NO SIGNAL IS DETECTED IN THE LIVER AND THE SIGNAL HAS DIMINISHED IN OTHER ORGANS. IT IS OBSERVED FOR THE FIRST TIME IN THE SHAUVARY GLAND, THYROLD GLAND AND WAS STRONG IN THE THYMUS, EYE,
                                                                                                                                                                                                                                                                                                                                                                                                             OLFACTORY EPITHELLUM AND CENTRAL NERVOUS SYSTEM. AT 1.5 DAYS AFTER BIRTH, THE EXPRESSION IS STILL STRONG IN THYMUS, BUT WEAKER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
-!- SUBUNIT: THE COLLED COLL C-TERMINUS REGION INTERACTS WITH AH
                                              -!- SUBCELLULIAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                     RECEPTOR NUCLEAR TRANSLOCATOR PROTEIN (ARNT) AND ARNT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.6%; Score 32; DB 1; Length 631;
83.3%; Pred. No. 75;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLED COIL (POTENTIAL).
MISSING (IN ISOFORM 2).
S -> SSHLSNSQ (IN ISOFORM 2).
P -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92D6324D3890E9CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPVWS -> PLCV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfur metabolite repression control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emericella nidulans (Aspergillus nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
70626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF156934; AAF85763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD25963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MORE LIMITED IN BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MG1:1341163; Tacc3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_Tax1D=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF093542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 DPQTHR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCONB OR MAPB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOB_EMENI
Q00659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPI.IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCOB_EMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

ö

Wed Aug 7 06:33:21 2002

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.6%; Score 32; DB 1; Length 678; 71.4%; Pred. No. 81; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                D840D452E37B4C53 CRC64;
                                                                                                                                                                                                                                   PROSITE; PS50181; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50082; WD_REPEATS_1; 4.
PROSITE; PS50094; WD_REPEATS_REGION; 1.
Transcription requiation; Repeat; WD repeat.
DOMAIN 178 224 F-BOX.
                                                                                                                                                                                                                                                                                                                    WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
                                                                                                                                                                                           PRINTS: PR00320; GPROTEINBRPT.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                76070 MW;
                                                                                                             EMBL; U21220; AAC15905.1; -. HSSP; P04901; 1GG2.
                                                                                                                                       InterPro; IPR001810: F-box.
InterPro; IPR001680: WD40.
Pfam; PF00646; F-box: 1.
Pfam; PF00400: WD40: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conservat
                                                                                                                                                                                                                                                                                                                                                                                      553
607
647
678 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11:1 |1
39 ETEPDTH 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
        ò
```

Search completed: August 7, 2002, 06:47:37 Job time: 209 sec

qq

```
August 7, 2002, 06:44:33 ; Search time 24.98 Seconds (without alignments) 55.403 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                   562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                562222 segs, 172994929 residues
                                                                                                                                                     US-1U-020-139-2_COPY_159_166
46
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match U%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sp_virus:*
sp_vertebrate:*
sp_vernclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                               1 ETUPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:*
                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                 Sedneuce:
                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9bqqQ homo sapien	ропо	O9led0 lycoparsico	_							O9sth6 arabidonsis						
ID	Q9BQQ0	Q96DR5	Q9LEG0	086975	022470	022471	09SVU3	98SS60	083393	0949M4	095ТН6	Q9SPG1	09PTJ2	09PAU9	022402	09LV72	
DB	4	4	10	12	10	10	10	10	15	10	10	10	13	16	10	10	
% Query Match Length DB	249	249	438	262	445	445	880	868	899	924	250	286	338	425	444	867	
% Query Match	100.0	100.0	84.8	82.6	80.4	80.4	78.3	78.3	78.3	78.3	76.1	76.1	76.1	76.1	76.1	76.1	
Score	46	46	6E	38	37	37	36	36	36	36	35	35	35	35	32	35	
Result No.	п	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	

17 34 73.9 178 19 34 73.9 178 19 34 73.9 178 22 34 73.9 1223 22 34 73.9 1223 22 33 73.9 1223 22 33 73.9 1223 22 33 71.7 1223 22 33 71.7 101 25 33 71.7 261 26 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 105 32 33 71.7 105 34 33 71.7 105 35 33 71.7 105 36 33 71.7 105 37 33 71.7 105 38 33 71.7 105 39 33 71.7 105 31 33 71.7 105 31 33 71.7 105 32 69.6 70 44 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 850000000000000000000000000000000000	09p039 homo sapien 02453 volvox cart 024532 volvox cart 0969v4 homo sapien 09115 homo sapien 090483 homo sapien 000029 acremonlum 000029 acremonlum 02170 atreptomyce 09bsp9 homo sapien 09274 cicer ariet 09364 arabidopsis 06574 cicer ariet 09364 arabidopsis 06574 cicer ariet 09364 arabidopsis 0631398 sphingomona 09491 homo sapien 09155 homo sapien 09155 homo sapien 09155 homo sapien 09154 mus musculu 091207 herpes simp 099007 herpes simp	A. update) EIN BSE	data; Cranlata; Vertebrata; Euteleostomi; dutes; Catarrhini; Hominidae; Homo. the EMBL/GenBank/DDBJ databases. 1;	249 AA. uence update) otation update)
17 34 73.9 178 19 34 73.9 178 19 34 73.9 178 22 34 73.9 1223 22 34 73.9 1223 22 33 73.9 1223 22 33 73.9 1223 22 33 71.7 1223 22 33 71.7 101 25 33 71.7 261 26 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 105 32 33 71.7 105 34 33 71.7 105 35 33 71.7 105 36 33 71.7 105 37 33 71.7 105 38 33 71.7 105 39 33 71.7 105 31 33 71.7 105 31 33 71.7 105 32 69.6 70 44 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 850000000000000000000000000000000000	0996039 0966B9 0966B9 0996B15 0996B15 0996B17 0998B17	Sz. Sz.	Cranlata; Catarrhii EMBL/GenBai : E64E079 Score 46 Pred. No 0; Mismatt	
17 34 73.9 178 19 34 73.9 178 19 34 73.9 178 22 34 73.9 1223 22 34 73.9 1223 22 33 73.9 1223 22 33 73.9 1223 22 33 71.7 1223 22 33 71.7 101 25 33 71.7 261 26 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 261 31 33 71.7 105 32 33 71.7 105 34 33 71.7 105 35 33 71.7 105 36 33 71.7 105 37 33 71.7 105 38 33 71.7 105 39 33 71.7 105 31 33 71.7 105 31 33 71.7 105 32 69.6 70 44 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 33 71.7 110 844 32 69.6 70 45 32 69.6 70 45 32 69.6 70 46 32 71.7 110 850000000000000000000000000000000000	22211 71 2 000224	17, 119, VINE	data the 11. 1 MW 108;	ത്ത്ത് -
17 34 19 34 19 34 19 34 19 34 19 34 19 34 19 34 122 34 22 34 22 33 22 33 22 33 22 33 22 33 22 33 32 22 33 33			Chor Prim 03546 2701 100 100 ative	·- H
17 19 19 19 19 19 20 20 20 20 20 20 20 33 33 33 33 33 33 33 33 33 33 33 33 33			M M N N N N N N N N N N N N N N N N N N	PREL (TrE (TrE (TrE (ETOR
O Ω Ε Ο Ο Ω Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο		1 9BQQ0 9BQQ0, 9BQQ0, 1-JUN-2001 1-DEC-2001 49G10.1. 749G10.1.	Malia; E Malia; E Mulchar Errario- DUENCE FR acey A.; acey A.; acey A.; DUENCE DUENCE Match Match Match Match 1 ETDPQT 1 I ETDPQT	2 96DR5 96DR5 1-DEC 1-DEC 1-DEC 1-DEC
		RESU QQBQ DD DD DD DD DD GN	<u>.</u>	RESUI 096DF 1D 1D AC DT DT DT DE OS

```
Pfam; PF00996; GDI; 1.
PRINTS; PR00891; RABGDIREP.
SEQUENCE 445 AA; 49701 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.v.
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Planta 210:143-149(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice)
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 EADPKTHQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 DVDPQTHQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ETDPQTHQ 8
                         STRAIN-7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                         Helicase.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     022471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      022470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            022471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            022470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
022471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         022470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
     0;
                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                 TISSUE-PAROTID:
Venkatesh S.G., Geetha C., Gorr S.-U.;
Vankatesh S.G., Geetha C., Gorr S.-U.;
Vankatesh S.G., Geetha C., Gorr S.-U.;
An member of the PSEV/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OGT-2001) to the EMBL/GenRank/DDBJ databases.
EMBL: AF412917; AAL28113.1: - FEMBL: AF412917; AAL28113.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barg R., Chmelnitsky I., Sobolev I., Salts Y.; "A tomato GDP dissociation inhibitor gene highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.8%; Score 39; DB 10; Length 438; 75.0%; Pred. No. 9.3; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 46; DB 4; Length 249; 100.0%; Pred. No. 0.21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-1996 (TrEMBLrel. 01, Last sequence update)
C-2001 (TrEMBLrel. 19, Last annotation update)
HELICASE-PRIMASE COMPLEX HOMOLOG PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ401079; CAB94202.1; -.
HSSP; P21856; ICND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 AA; 48728 MW; B51E7E02D96DC2A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phocid herpesvirus 2.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDP DISSOCIATION INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002005; Rab_GDI_REP. Pfam; PF00996; GDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0891; KABGDIREP.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Frac 6; Conserva
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 ETDPQTHQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ETDPKTHE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=47419;
                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_Tax ID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      086975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSTEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  086975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UL52'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             086975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09LEG0
```

SO DE RETAR SO DE RETAR SO DE RETAR SE SO DE RETAR SE SO DE RETAR SO DE RETAR

g

ô

a

DA SOS SE

ò

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                Harder T.C., Harder M., Vos H., Kulonen K., Kennedy-Stoskopf S., Liess B., Appel M.J., Osterhaus A.D.; "Characterization of phocid herpesvirus-1 and -2 as putative alpha-and gammaherpesviruses of North American and European pinnipeds."; EMBL; S81230; AAB35973.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20059514; PubMed-10592042; Kim M.Y., Kim C.Y., Cheong N.E., Choi Y.O., Lee K.O., Lee S.H., Park J.B., Nakano A., Bahk J.D., Cho M.J., Lee S.Y.; "Characterization of two fungal-elicitor induced rice cDNAs encoding functional homologues of the rab-specific GDP-dissociation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                             ·;
                                                                                                                                                                                                                                                                                                                                                                   82.6%; Score 38; DB 12; Length 262; 75.0%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.4%; Score 37; DB 10; Length 445; 75.0%; Pred. No. 24; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA; 49701 MW; 09EEC9101849F9D3 CRC64;
                                                                                                                                                                                                                                             NON_TER 1 1
SEQUENCE 262 AA; 30101 MW; 83AA01A8BB6D2790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GDP DISSOCIATION INHIBITOR PROTEIN OSGDI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
MEDLINE-96145132; Pubmed-8558126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1PR002005; Rab_GDI_REP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF016896; AAB69870.1; -.
HSSP; P21856; IGND.
```

Eukaryota; Viridiplantae; Streptophytà; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. "Complete Nucleotide Sequence of mouse mammary tumor virus from JYG chinese wild mice: absence of bacterial insertion sequences in the cloned viral gag gene."; -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS (BY SIMILARITY). MEDLINE-87112944; PubMed=3027377;
Moore R., Dixon M., Smith R.E., Peters G., Dickson C.;
"Complete nucleotide sequence of a milk-transmitted mouse mammary tumor virus: Two frameshift suppression events are required for translation of gaq and pol.";
J. Virol. 61:480-490(1987). Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremenetskala I., Kim C., Lanz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskala V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (SEP-1999) to the EMBL/CenBank/DDBJ databases. EMBL, AC009322; AAD5478.1; Nishio M., Xu L., Sasaki M., Haga S., Okumoto M., Mori N., Sarkar N.H., Acha-orbea H., Enami J., Imai S.; POL OR GAG-POL OR GAG PRO POL. Mouse mammary tumor virus. Viruses: Retroid viruses: Retroviridae; Betaretrovirus. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Arabidopsis thaliana (Mouse-ear cress). 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last segu 01-DEC-2001 (TrEMBLrel. 19, Last anno GAG PRO POL POLYPROTEIN (FRAGMENT), F18B13.31 PROTEIN (FRAGMENT). EMBL; D16249; BAA03767.1; -. HSSP; P03355; 1MML. :89-94(1994). Conservative PRELIMINARY; PRELIMINARY; SEQUENCE 898 AA; Best Local Similarity Matches 6; Conserv SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCB1_TaxID=11757; 46 ETLPQTHQ 53 PubMed=11091515; NCB1_TaxID-3702; Breast Cancer 1 47 TDPQTH 52 2 TDPQTH 7 Query Match 083393; **988860** 083393 ဆ σ RESULT RESULT 083393 a ò a 0; . 0 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis. Kim W.Y., Kim C.Y., Cheong N.E., Choi Y.O., Lee K.O., Lee S.H., Park J.B., Nakano A., Bahk J.D., Cho M.J., Lee S.Y.; "Characterization of two fungal-elicitor-induced rice cDNAs encoding functional homologues of the rab-specific GDP-dissociation inhibitor."; Gaps Gaps Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza ., Jarke D., Scharfe M., Schon O., Mewes H.W., 0 0 80.4%; Score 37; DB 10; Length 445; 75.0%; Pred. No. 24; Query Match 78.3%; Score 36; DB 10; Length 880; Best Local Similarity 87.5%; Pred. No. 75; Matches 7; Conservative 0; Mismatches 1; Indels Bevan M., Brandt P., Dose S., Jarke D., Scharfe M., Schon Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDbJ dalabases. 1; Indels SEQUENCE FROM N.A. Brank D., Scharfe M., Schon O., Mewer Brandt P., Dose S., Jarke D., Scharfe M., Schon O., Mewer Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. 1; Indels EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ALU35353; CAA22976.1; -.. EMBL; ALI61573; CAB81464.1; -.. EU Arabidopsis sequencing project; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases 445 AA; 49559 MW; F3F01C989AEEC277 CRC64; 98423 MW; SFD1102587BCBBF0 CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 98.4 KDA PROTEIN.
F16A16.130 OR AT4G28760. 880 AA. 1; Mismatches PRT; MEDLINE-20059514; PubMed-10592042; EMBL: AF016697; AAB698711; -. HSSP; P21856; IGND. HTG-FPC: PR002005; Rab_GDI_REP. Pfam; PF00996; GDL: 1. PRINTS; PR00891; RABGDIREP. Ouery Match
Best Local Similarity 75...
6, Conservative 10:143-149(1999). PRELIMINARY; Hypothetical protein SEQUENCE 880 AA; SEQUENCE FROM N.A. SECUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=4530; NCBI_TaxID=3702; 1 ETDPOTHQ 8 1 ETDPOTHQ 8 SEQUENCE Planta 2 09SVU3

RESULT 09SVU3

â

ò g ·;

Gaps

;

0; Indels

0; Mismatches Pred. No.

100.08;

Last sequence update)
Last annotation update)

PRT; 899 AA.

78.3%; Score 36; DB 10; Length 898; 100.0%; Pred. No. 77;

100942 MW; 7BEF47EA09673E3C CRC64;

PRT;

020 137-2_COPY_137_100.15PC

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermalophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     T4C9.190 OR AT4G12350.
                                                                     NCB1_Tax10=3702;
     ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
Yamada K., Liu S.X., Pham P.K., Isee J.M., Onodera C.S., Quach H.L.,
Goldsmith A.D., Jtang P.X., Isee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
Carninci P., Chen H., Chenk K., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
Lin J., Mayers M.C., Miranda M., Natursaka M., Nquyen M., Palm C.J.,
Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Tracy S.E.,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
"Full Length CDNA of gene AT4928760 (GI: 2269731).";
Submitted (GUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                               :
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                               Pfam; PF0065; rve; 1.
Pfam; PF00678; rvt; 1.
DNA-binding; Endonuclease; Hydrolase; Nucleotidyltransferase; Polyprotein; RNA-directed DNA polymerase.
NON_TER 1 1 1 1 1 SEQUENCE 899 AA; 102359 MW; A78C4F65FF77AA TOTALA
                                                                                                                                                                                                                 78.3%; Score 36; DB 15; Length 899; 75.0%; Pred. No. 77; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.3%; Score 36; DB 10; Length 924; B7.5%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY051010; AAK93687.1; -...
Hypothetical protein.
SEQUENCE 924 AA; 102903 MW; 10B55CC87876CA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           1-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0JN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                  924 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  PRT;
               Integrase_zn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
InterPro; IPR001037; Integrase_C.
                                                             Pfam; PF00552; Integrase: 1. Pfam; PF02022; Integrase_2n; 1. Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL 102.9 KDA PROTEIN.
                           KNaseH.
            InterPro, IPR003308; Integr.
InterPro, IPR002156; KNaseH
InterPro, IPR001584; Rve.
InterPro, IPR000477; RVTse.
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

Best Local Similarity 87.5,

Conservative
7,
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                              873 ETDPRPHQ 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ETLPQTHQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                      1 FTDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                 0949M4;
                                                                                                                                                                                                                                                                                                                                                                  0949M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09STH6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
Q9STH6
ID Q9STH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9H1S60
                                                                                                                                                                                                                                                                                                                                        RESULT 10
 q
                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC
DT
DT
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                          Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
Bancroft J., Mewes H.W., Mayer K.F.X., Lemcke K., Mannhaupt G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.1%; Score 35; DB 10; Length 250; 75.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL080318; CAB45882.1;
EMBL; AL161533; CAB78278.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostro, PEO0239; myb_DNA-binding; 2. SMART; SM00395; SANT; 1. PROSITE; PS00334; MYB_2; 1. PROSITE; PS50090; MYB_3; 1. SROUENCE 250 AA; 28231 MW; D97D7A56Al3D8AB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21481677; PubMed=11597504;
Stracke R., Werber M., Weisshaar B.,
The R2R3-WB gene family in Arabidopsis thaliana.";
Curr. Opin. Plant Biol. 4:447-456(2001).
EMBL; AF175999; AAD53104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMIT PROGRAS, MY_DUA_DUA_DIA_U.S. SMART. SM0395; SANT; 2. PROSTITE; PS0037 WYB_L! UNKNOWN_I.PROSTITE; PS00334; WYB_2; 1. PROSTITE; PS50090; MYB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSE; USSES; TOTO.
InterPro; IPR001005; Myb_DNA_bind.
NETT: DE00749: mvb DNA-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001005; Myb_DNA_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q03237; 1A5J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01103; 1POM.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 11 ||1|
| 84 EIDPSTHU 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ETDPQTHQ 8
                                                                                      Schueller C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBSPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
```

SEQUENCE Query Match 022402 RESULT 15 022402 qq A 5 .. O 0 Reiter J.F., Zon L.I., Stainier D.Y.R.; "Zebrafish gata4 and gata6 are expressed in the heart and endoderm."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AF191577; AAF15275.1; -. HSSP; P17679; 1GNF. 0; Gaps Gaps Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopteryqii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; .. 76.1%; Score 35; UB 13; Length 338; 75.0%; Pred. No. 44; Score 35; DB 10; Length 286; 2;. Indels 2; Indels PRINTS FACCULAR GATA: 2.

SMART: SMOUGOL: ZAF GATA_ZA_FINGER_1: 2.

PROSITE: PS00344; GATA_ZA_FINGER_1: 2.

PROSITE: PS50114; GATA_ZA_FINGER_2: 2.

PROSITE: A38 AA: 36922 MW: 862F278C445AAAIF CRC64; 286 AA; 32402 MW; A266805A0£784A61 CRC64; 01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Brachydanio rerio (Zebrafish) (Zebra danio). 338 AA 425 AA 0; Mismatches 0; Mismatches 37; ZINC FINGER TRANSCRIPTION FACTOR GATA4. Pred. No. · PRT'; MEDLINE=20365717; PubMed=10910347; P17679; IGNF. ZDB-GENE-980526-476; gata4. InterPro; IPR000679; ZnF_GATA. InterPro; IPR001164; Znf_GCS. Pfam; PF00320; GATA; 2. PRINTS; PRO0619; GATAZNFINGER. 76.18; Conservative 6; Conservative PRELIMINARY; PRELIMINARY; Xylella fastidiosa. Query Match Best Local Similarity Best Local Similarity SEQUENCE FROM N.A. 293 EKDPDTHQ 300 120 EIDPSTHQ 127 AMINOTRANSFERASE. NCBI_TaxID=2371; NCBI_TaxID=7955; 1 ETDPOTHQ 8 1 ETDPOTHQ 8 STRAIN-9A5C Query Match SEQUENCE 09PAU9; Q9PTJ2 Q9PAU9 RESULT 13 RESULT 14 Matches Matches Q9PTJ2 Q9PAU9 g S ô

```
Ezaki B., Koyanagi M., Gardner R.C., Matsumoto H.; "Nucleotide sequence of cDNA for a GDP dissociation inhibitor (GDI) which is induced by aluminum (Al) ion stress in tobacco cell culture (Accession No. AF012823) (PGK97-133).";
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Nicotiana.
"The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                            Score 35; DB 16; Length 425; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 35; DB 10; Length 444; 62.5%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                   425 AA; 46381 MW; 5B1A2C657AFC39E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 AA; 49702 MW; 5484214FAD3773D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 AA
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                 InterPro, IPR001176; ACC_synthase.
PRINTS; PR00753; ACCSYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002005; Rab_GDI_REP. Pfam; PF00996; GDI; 1. PRINTS; PR00891; RABGDIREP.
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AFÖ12823; AAB80717.1; ·.
HSSP; P21856; 1GND.
                                                             EMBL; AE004048; AAF85195.1; -.
                                                                                                                                                                                                                                               76.18;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDP DISSOCIATION INHIBITOR
                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 85,/*
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                       Complete proteome.
SEQUENCE 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. SAMSUN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                       71 TDPYTHO 77
                                                                                                                                                                                                                                                                                                                                                       2 тъготно в
```

us-10-020-139-2_COPY_139_100.18PC Med Aug / 00:33:22 2002

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Oy 1 ETDPQTHQ 8 |:||:||: |DD 151 ESDPKTHE 158

Search completed: August 7, 2002, 06:48:10 Job time: 217 sec

```
Med Aug / U0:33:10 2002
```

us-10-020-139-2_copy_toy_tob.rag

raher

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 7, 2002, 06:43:38 ; Search time 29.84 Seconds Run on:

(without alignments) 29.778 Million cell updates/sec

US-10-020-139-2_COPY_159_166

Perfect score:

1 ETDPQTHQ 8 **BLOSUM62** Scoring table: Seguence:

747574 seqs, 111073796 residues Searched:

Gapop 10.0 , Gapext 0.5

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

/sibsi/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/sibsi/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1988.DAT:*
/sibsi/gcgdata/hold-geneseqy-embl/AA1988.DAT:* /SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*/SIDSI/gagdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1990.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:* /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1994.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:* /SIDS1/gcgdata/hold-geneseg/geneseqp-embl/AA1996.DAT:* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1993.DAT: A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Ouery Match Length DB	DB	ID	Description
	46	100.0	50	22	ABB41435	Peptide #8941 enco
7	46	100.0	50	22	AAM62308	Human brain expres
e	46	100.0	50	22	AAM75111	Human bone marrow
ŧ.	46	100.0	50	22	AAM35227	Peptide #9264 enco
5	46	100.0		19	AAW69221	Human parotid secr
9	46	100.0		19	AAW60682	Human parotid secr
7	46	100.0		21	AAB24069	Human PRO1025 prot
œ	46	100.0		21	AAB25765	Human secreted pro
σ	46	100.0	249	22	AAB75351	Human secreted pro
10	41	89.1		22	AAM25745	Human protein segu
11	36	78.3		22	ABG25271	Novel human diagno

l human dia	el human	el human dia	el human dia	el human dia	al human dia	human dia	l human dia	l human dia	l human di	1 human d	l human di	1 human d	l human di	l human d	human d	_	human d	el human d	el human dia	l human dia	l human d	l human dia	n peptide #		ein #60	brain e	bone mar	ide #6	ide #63	ide #608	L human dia	l human di
Nove	ON ON ON	NON	NOV	Nov	NOV	Nove	Nove	Nove	Nove	Nove	Nove	Nove	Nove	Nove	Nove	Nove	Nove	NOV	NOV	NOV	Nove	Nove	Huma	Pep	Pro	Humai	Humar	bep	Pept	beb	Nove	Nove
ABG06840	00000	328	32	₹	30		ABG00609	307	583	378	328	27	526	526	505	ABG19795	327	328	163	583	328	9	96,	313	9	393	332	119	AAM26600	192	ABG06242	092
22	22	222	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
119	VΨ	œ	5	0	7	9	9	9	9	7	0	ᆏ	\vdash	S	5	S	S	9	9	æ	0	4	~	1	^	~	478	7	~	^	511	~
78.3	ο α	 	ω ω	8	&	ω	&	ش	8	œ	œ	ъ Э	8	æ	œ	ж Ж	ω.	8	8	œ.	8	8	œ	œ	8	ω.	ထ	œ	ω ω	ω ω	ω ω	œ
36	o ve	o	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	. 9	9	9	9	9	9	90	9	9	9
12	74		16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45

ALIGNMENTS

Peptide #8941 encoded by human foetal liver single exon probe. ABB41435 standard; Peptide; 50 AA. 04-FEB-2002 (first entry) ABB41435; RESULT ABB41435

Human; foetal liver; gene expression; single exon nucleic acid probe.

WO200157277-A2.

09-AUG-2001

2000US-0180312. 2000US-0207456. 2000US-0608408. 03-AUG-2000; 2000US-0632366. 21-SEP-2000; 2000US-0234687. 27-SEP-2000; 2000US-0236359. 30-JAN-2001; 2001WO-US00669. 04-OCT-2000; 2000GB-0024263. 04-FEB-2000; 26-MAY-2000; 30-JUN-2000;

(MOLE-) MOLECULAR DYNAMICS INC

Rank DR; Hanzel DK, Chen W, Penn SG,

WPI; 2001-483447/52.

```
epilepsy and cancers. The present sequence is a protein encoded by one of
                            the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                           50 AA;
                                                                                                                                                                                                                                                                                              22. et.dpqthq 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 etdpqthg 29
                                                                                                                                                                                                                                             1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ETDPOTHO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM75111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                               AAM75111
                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\
  000×8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The passent invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases quch as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                                                                                                 liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                               measuring human gene expression in a sample derived from human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 34413; 650pp + Sequence Listing; English.
                                                                                                                     The invention relates to a single exon nucleic acid probe for
                                                                      Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17; Live 0; Mismatches 0; Indels
                       analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM62308 standard; Protein; 50 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
7-SEP-2000; 2000US-0234597.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 etdpgthg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM62308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AAM62308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
ολ
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 35417; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; cancer; leukaemia; lymphoma; myeloma.
                          100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SC, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                AAM75111 standard; Protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MP1; 2001-488900/53.
                                Best Local Similarity
Matches 8; Conserve
```

```
Homo sapiens.
                                                                                                                                                       23-DEC-1996;
                                                                                                                                 18-DEC-1997;
                                                                                         WO9828420-A1
                                                                                                               02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW60682;
                                      Peptide
                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW60682
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AAI31315.AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                      Peptide #9264 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 46; DB 22; Length 50; 100.0%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                            Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW69221 standard; Protein; 249 AA.
                         AAM35227 standard; Protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parotid secretory protein.
                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0214687.
27-SEP-2000; 2000US-0214687.
                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663.
                                                                 17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
.^^ 8; Conserve
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 AA;
                                                                                                                    genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 etdpgthg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ETDPQTHQ 8
                                                                                                                                                             WO200157272-A2.
                                                                                                                                          Homo sapiens.
                                                                                                                                                                                 09-AUG-2001.
                                              AAM35227;
                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW69221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŋ
             AAM35227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW69221
     RESULT
                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
```

```
This sequence is the human parotid secretory protein (hPSP) of the invention. The hBSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hBSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, on-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hBSP. The protein is pancreas which are associated with high levels of hBSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (b), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with expessive hBSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for the DNA are used to contain and this can be used to raise Ab, useful and this can be used to raise Ab, useful and this can be used to raise Ab, useful and the account of the protein and this can be used to raise Ab, useful and the account of the protein and this can be used to raise Ab, useful and the account of the protein and this can be used to raise Ab, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal tissue; HPSP; Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 46; DB 19; Length 249; 100.0%; Pred. No. 0.91; ive 0; Mismatches 0; Indels (
                                                                     /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parotid secretory protein (HPSP).
                                                                                                                                                                       "mature hPSP"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW60682 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0034429.
                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US23522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv....
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1998 (first entry)
                                                                                                                                  249
                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duan R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 etdpgthg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV44759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ETDPQTHQ 8
```

```
W0200053755-A2.
                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB25765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
 ŏ
                                                                                                                                                                                                                                                                                                                                                                 that bind specifically to, and modulate activity of HPSP, integolitzes, that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, or gastrointestinal tract or pancreas. Sjorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to produce recombinant HPSP which is used to generate antibodies and to produce recombinant HPSP which is used to generate antibodies and to antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunosuppressive; immunosuppressive; neuronal disorder; antianalogenic; leukaemia; lymphoid malianancy; hypothalamic disorder; glandular disorder; macrophagal disorder; proferientelial disorder; strong disorder; blastocoelic disorder; inflammatpry disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                        This represents a human parotid secretory protein (HPSP). Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                               New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ulcerative colitis; Crohn's disease; atrophic qastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB24069 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1A-C; 65pp; English.
                                                                                                             97WO-US20651.
                                                                                                                                       96US-0749288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0
Matches 8: Conservative
                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                Bandman O, Goli SK;
                                                                                                                                                                                                                          WPI; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB: AAV37699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ETDPQTHQ 8
                                                     WO9821329-A1.
                           Homo sapiens.
                                                                                                             07-NOV-1997;
                                                                                                                                       14-NOV-1996;
                                                                                 22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB24069
                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
```

```
The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0390, PR0311, PR0315, PR01005, PR0117, PR08109, PR01105, PR01105, PR011009, PR01005, PR01005, PR01005, PR01005, PR01005, PR01005, PR010184, PR010187, PR021080, PR02196, PR02197, PR01111, PR01187, PR021084, PR02197, PR02111, PR01187, PR021084, PR02198, PR02198, PR08145, PR02191, PR02198, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 46; DB 21; Length 249; 100.0%; Pred. No. 0.91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,
,
                                                                                                                                                                                                                                                                                 99US-0143048.
99US-0145698.
99WO-US28313.
                                                                               2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US30911.
                                                                                                                                                               99WO-US05028
                                                                                                                                                                                                                                          99US-0141037
                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-2000; 2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 etdpgthg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ,
                                                                           06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe CK,
                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                                                                                                              26-JUL-1999;
                                                                                                                                                                                                                                                                                      07-JUL-1999;
14-SEP-2000.
                                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB25765;
```

```
Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
Antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
Antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
Antiarty; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
Antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
Antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; czema;
Antiaggregant; haemostatic; vulnerary; antidiabetic; cytostatic;
Antiagregant; neufactic; antidapetic; osteopathic; czema;
Antianaphylactic; rheumatory; antisense therapy; vaccine; inflammation;
Antianaphylactic; rheumatorid arthritis; septic shock; pancreatitis;
Antianaphylactic; rheumatopology; cardiac anaphylaxis; autoimmunity;
Antianaphylactic; antiparty; severe combined immunodeficiency;
Antianaphylactic; diabetes; multiple sclerosis; depression;
Antianaphylactic; antiparty; severe combined immunodeficiency;
Antiparty of disease; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to 49 Secreted proteins and the CDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 Secreted proteins and the nucleic acids encoding them, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 46; DB 22; Length 249; 100.0%; Pred, No. 0.91; tive 0; Mismatches 0; Indels C
                                                                                                                                     Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy and for detecting similar sequences in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards J, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0469099
                            05-APR-2001 (first entry)
                                                                                     Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-071487/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 etdpgthg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                    WO200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1999;
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                       04-JAN-2001
                                                                                                                                                              infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM25745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                             Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis, hyporhyvoidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondricoytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAAB7725.AB774 which encode human secreted proteins AAB25763-B25612. The proteins include signal peptides included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequences, and a purified antibody capable of binding to one of the storing the sequence data on a computer system, and a method for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodics capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, amyloidosis, brain disorders, skeletal muscle disorders, gradiant disorders, deseity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemla, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 46; DB 21; Length 249; 100.0%; Pred. No. 0.91; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disorders, cystic fibrosis, hypothyroidism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75351 standard; protein; 249 AA.
                                                     Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0141032
28-NQ-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                    septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 etdpqthg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA87727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ETDPOTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                        WO200037491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2000.
```

Sednence

Query Match

AAB75351;

0

g ò

ö

Gaps

ó

WO200175067-A2.

11-OCT-2001

```
AMA29466 to AAH99904 encode the human proteins given in AAM2525 to
CC AAM25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antiinflammatory; antitheumatic;
calls they are expressed in, such as: antiinflammatory; antitheumatic;
antiathritic; immunosuppressive, antibacterial; endocrine, cardiant;
cardiovascular; antianaemic; antiaggeant, hemosatatic; vulnerary;
cardiovascular; antianaemic; antiaggeant, naminatic; untidiabetic; osteopathic; dermatological; antiallerage; antiasthmatic;
antidiabetic; osteopathic; neuroprotective; antidepressant; nootropic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
contigations in and immunostimulant. The proteins and polynucleotides
concoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used with the activity of a protein e.g. inflammation,
confecuency, septic shock, pancerealtis, cardiac dysfunction,
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fuggal
infections, autoimmunity, quentic diseases, hemmatopoietic disorders,
anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
conteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple solerosis, depression,
animalianal diseases, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                    Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.1%; Score 41; DB 22; Length 260; 100.0%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #25262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG25271 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.10,
100.0%; Pre
                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT;
                                                                                                                    22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                      25-APR-2000; 2000US-0552317.
                                                                                                                                                                99US-0471275
                                                                                                                                                                                  21-JAN-2000; 2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorders.
                                                                                                                                                                                                                                                                                                                           2001-457603/49.
                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 etdpgth 176
                                     WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ETDPQTH 7
Homo sapiens.
                                                                                                                                                            23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG25271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG25271
                                                           Οy
```

```
polypeptide (II) sequences. (II) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in dispnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.3%; Score 36; DB 22; Length 88; 85.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (1) and
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ 1D No 55630; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #6831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG06840 standard; Protein; 119 AA.
                                                                                                                                                                                                                   Tang YT;
                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Overy Match
Best Local Similarity 85...
6: Conservative
                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AA;
                                                                                                                                                                                                                                                                         N-PSDB; AAS89458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 111
32 tdpdthg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 трротно 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG06840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG06840
ò
```

```
30-MAR-2001; 2001WO-US08631.
11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG23981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG23981
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polypurcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WTPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; indels
                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred, No. 29;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                               Claim 20; SEQ 1D No 37199; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.3%; Score 36;
85.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #4621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG04630 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                        30-MAR-2001; 2001WO-US08631.
                                                                               23-AUG-2000; 2000US-0649167.
                                                                31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 119 AA;
                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 tdpdthg 100
                                                                                                                                                                       N-PSDB; AAS71027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                          biodiversity
              11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                     ò
```

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome can gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human cald sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 34989; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; Score 36;
85,7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #23972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG23981 standard; Protein; 161 AA.
                                                                                                                                                                                                   Tang YT;
31-MAK-2000; 2000US-0540217.
                                           23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AA;
                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS68817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 tdpdthq 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 треотно в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
```

30-MAR-2001; 2001W0:US08631

```
for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Conter: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; Score 36; DB 22; Length 161; 85.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 54340; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #23275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG23284 standard; Protein; 181 AA.
                                                                                                                                                                                 Tang YT;
                                                                2000US-0540217.
2000US-0649167.
                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.33
Best Local Similarity 85.73
Matches 6; Conservative
                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                           WPI: 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 161 AA;
                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                       N-PSDB; AAS88168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 tdpdthg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO20017,5067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                   biodiversity
                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG23284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG23284
ò
```

```
polypeptide (II) sequences to isolated polyputicitie (I) and polypeptide (II) sequences (I) brinders, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polyputicities are also used in diagnostics as expressed sequence tags to identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging observant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Absolute Adds 30377 represent novel human and amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 36; DB 22; Length 181; 85.7%; Pred. No. 45; atlive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 53643; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 7, 2002, 06:45:27
                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                  WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 181 AA;
                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 tdpdthq 131
                                                                                                                                                                                                                                         N-PSDB; AAS87471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TUPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time:
```

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1190, Ap
Sequence 1192, Ap
Sequence 1193, Ap
Sequence 1194, Ap
Sequence 1200, Ap
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
                                                             August 7, 2002, 06:43:38; Search time 12.96 Seconds (without alignments) 15.078 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appl
Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    App1
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/FDUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/FDUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-1017-205-52
US-08-159-339A-1190
US-08-159-339A-1194
US-08-159-339A-1194
US-08-159-339A-1194
US-08-159-339A-1200
PCT US-95-15696-2
US-08-95-15696-3
US-08-917-965-76
US-08-917-968-10
US-08-801-973-2
US-08-801-973-2
US-08-811-107-10
US-08-46-793-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-914-999-18
US-08-914-999-15
US-08-914-999-16
US-08-773-870-5
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-914-999-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-017-205-51
                                                                                                                                                                                       231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                          US-10-020-139-2_COPY_159_166
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                 1 ETDPQTHQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2257
209
212
233
238
238
258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391
425
425
675
732
732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1456
                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                      Scoring table:
                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                   Sednence:
                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
9
```

```
ö
                          Sequence 8, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 2, Appli
                                                                             Appli
                                                                                       1189, Ap
29, Appl
                                                                                                          , Appl
                                                                                                                               Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                    Sequence 2,
                                                                             Sequence Sequence 1
                                                                                                                                        Sequence 3
                                                                                                                     Sequence
                                                                     Sednence
                                                                                                           Sequence
                                                                                                                                                                      Sequence
                                                                                                   Seguence
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.6%; Score 32; DB 2; Length 18; 83.3%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                   :: Nixon & Vanderhye PC
8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide from HSV-2 glycoprotein G internal
                         Mismatches
                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMBER: US/09/017,205
02-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  Sequence 51, Application US/09017205; Patent No. 5965357; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
amino acid
540
724
725
732
760
768
803
1146
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                     Arlington
                                                                                                                                                                                                                                                                                                                                                                 Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02
CLASSIFICATION:
000000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||:||
13 TDPKTH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TDPQTH 7
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 8
                                                                                                                                                                                                                                          US-09-017-205-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-017-205-51
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
STATE:
```

```
Wed Aug / Ub:33:1/ 2002
```

1RM Compatible

us-10-020-139-2_copy_139_100.1al

```
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
.
                                                                                    APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%; Score 32; DB 2; Length 18; 83.3%; Pred. No. 6.2; trive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA Binding peptides and Their
                                                                                                                                                                                             ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal
US-09-017-205-52
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                ...eek: US/09/017,205
02-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1190, Application US/08159339A Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604-436
                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                       Seguence 52, Application US/09017205 Patent No. 5965357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)816-4000
(703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)010
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
FRIGHT: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 83.3° tes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
3Y: linear
                                                                                                                                                                                                                                                        Virginia
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22201-4714
                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                    Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-159-339A-1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TDPKTH 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                        US-09-017-205-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%; Score 31; DB 3; Length 9; 71.4%; Pred. No. 1.7e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kubo, kalph F.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
APPLICANT: CELIS, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
UMBER: US/08/159,339A
29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1192, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-NOV-1993 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
                                                                                                                                                     FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                     1190:
                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: TWO LILLS
CITY: San Francisco
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                  FILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-159-339A-1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ETDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ETDPTSH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-159-339A-1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
```

ö

```
0;
                                                                                                                                                                                                                      67.4%; Score 31; DB 3; Length 9; 71.4%; Pred. No. 1.7e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA Binding peptides and Their
Uses
: 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/159,339A
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECLIBERATION NUMBER: 32,762
REPRENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICK APPLICATION DATA:
APPLICATION NUMBER: US U7/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MA-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1194, Application US/08159339A ; Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1194: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM Compatible
                                                                                                                                                                                                                                             Best Local Similarity 71.4
Matches 5; Conservative
           INFORMATION FOR SEQ ID NO:
                               SEQUENCE CHARACTERISTICS:
                                                    9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                             single
                                                                                                               ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-159-339A-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-159-339A-1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            1 ETDPQTH 7
                                                                                                                                                                                                                                                                                                                                                   1 ETDPTSH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-159-339A-1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                               LENGTH:
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.4%; Score 31; DB 3; Length 9; 71.4%; Pred. No. 1.7e+05; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kubo, Raiph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SQUENCES: 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Grew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MDDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELERAX: (415) 576-0300
TELEX:
                                                                                                                                 REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-A02-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1193, Application US/08159339A Patent No. 6037135
                                                                                                                                                                                                                                          INFORMATION FOR SEQ 1D NO: 1192:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.44.
5, Conservative
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-159-339A-1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ETDPTSH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-159-339A-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

67.4%; Score 31; DB 3; Length 9;

Query Match

```
Query Match 67.4%; Score 31; DB 5; Length 391; Best Local Similarity 71.4%; Pred. No. 2.3e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                              APPLICANT: President and Fellows of Harvard College
TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
ITILE OF INVENTION: CELL DIVISION REGULATORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HU-9404 WO
                                                                                                                                                                                                                                                                                                                                                                       Farrell, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORREY AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: HJ. 94
TELECOMMUNICATION INFORMATION:
TELEFAN: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/08951148
; Patent No. 5871973
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                          ADDRESSEE: Kevin M. F
STREET: P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                            STREET: P.O. BOX CITY: York Harbor
        GENERAL INFORMATION:
APPLICANT: Presid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 TDPUPHK 314
                                                                                                                                                                         Maine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TDPQTHQ 8
                                                                                                                                                                                                              03911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-15696-2
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-951-148-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                            Gaps
                            .
0
Best Local Similarity 71.4%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.4%; Score 31; DB 3; Length 9; 71.4%; Pred. No. 1.7e+05; atlive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                          APPLICANT: Kubo, Ralph T.
APPLICANT: Kubo, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Cerlis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 321

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300
                                                                                                                                                                                                   Sequence 1200, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US 07/926,666
07-AUG-1992
UMBER: US 08/027,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application PC/TUS9515696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-159-339A-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                    ||||| :|
| ETDPASH 7
                                                            1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                US-08-159-339A-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ETDPTSH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ETDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-15696-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                               ò
                                                                                                    Q
```

Gaps

```
0; Gaps
                                                                                                                                                                                                                                             67.4%; Score 31; DB 2; Length 425; 71.4%; Pred. No. 2.5e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.4%; Score 31; DB 3; Length 425; 71.4%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: EastSog for Windows Version 2.0
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/09/274,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0407 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,148
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-274-570-3
; Sequence 3, Application US/09274570
; Patent No. 6121019
        INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 amino acids
                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                          ; LIBRARY: LVZNNOT01
; CLONE: 348429
US-09-165-234-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVZNNOT01
                                                                                                        linear
                                                                   amino acid
                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASS (FICATION:
                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: LVZNN
CLONE: 348429
                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                              67 ESDPATH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        1 ETDPOTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-274-570-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.4%; Score 31; DB 2; Length 425; 71.4%; Pred. No. 2.5e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
NUMBER: OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0407 US
APPLICATION NUMBER: US/08/951,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/951,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09165234
Patent No. 5928899
                                                                                                                             REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855.0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORNEY/AGENT .... NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                : 425 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%
Matches 5; Conservative
                  FILING DATE: Herewith
                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                       ; IMMEDIATE SOURCE:
; LIBRARY: LVZNNOT01
; CLONE: 348429
US-08-951-148-3
                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 ESDPATH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ETDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-165-234-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
```

ö a

Matches

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GONZALEZ C.
APPLICANT: GONZALEZ C.
APPLICANT: Lange, B.
APPLICANT: Lange, B.
TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE TITLE OF INVENTION: CORPRESSORE
CURRENT APPLICATION NUMBER: US/09/307,143
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                           67.4%; Score 31; DB 3; Length 676;
71.4%; Pred. No. 4.1e+02;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%; Score 31; DB 4; Length 724; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 210121.420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBER: US/08/533,669A
22-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/U8533669A
Patent No. 5834592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09307143
; Patent No. 6335157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                ; TYPE: PRT
; ORGANISM: Bacillus sp.
US-08-947-965-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-307-143-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserva
                                                                                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 65.c.
TTTY: Seattle
                                                                                                                                                                                                                                                           259 EVDPQNH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22
CLASSIFICATION:
                                                                                                                                                                                                                  1 FTDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 DPQTH 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-533-669A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                    US-09-307-143-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT.
                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
         ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                      Sequence 76. Application US/08947965A

Patent No. 6004790

GENERAL INFORMATION:
APPLICANT: Dijkstra, Bauke
APPLICANT: Dijkstra, Bauke
APPLICANT: Dijkstra, Grassen
TITLE OF INVENTION: Carsten
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
TITLE OF INVENTION NUMBER: US/08/947,965A
CURRENT FILING DATE: 1995-04-21
EARLIER PILING DATE: 1995-10-17
EARLIER PILING DATE: 1995-10-17
EARLIER PILING DATE: 1996-04-22
NUMBER OF SEQ ID NOS: 78
SEQ ID NOS: 78
SEQ ID NOS: 78
SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.4%; Score 31; DB 3; Length 675; 71.4%; Pred. No. 4e+02; tive 0: Mismatches 2; Indels
       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Dijkbuizen, Lubbert
APPLICANT: Dijktuizen, Lubbert
APPLICANT: Andersen, Carsten
APPLICANT: Osten, Claus von der
APPLICANT: OSten, Claus von der
ATTLE OF INVENTION: Oglomaltodextrin Glucanotransferase
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 4285.204.US
CURRENT APPLICATION NUMBER: US/08/947,965A
CURRENT PILING DATE: 1997-10-09
BARLIER PELING DATE: 1997-04-21
EARLIER FILING DATE: 1995-04-21
EARLIER FILING DATE: 1995-10-17
EARLIER FILING DATE: 1995-10-17
EARLIER FILING DATE: 1995-10-17
EARLIER FILING DATE: 1995-10-17
EARLIER FILING DATE: 1995-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/08947965A
Patent No. 6004790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRCANISM: Bacillus Obbensis
US-08-947-965-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 71.4%
For S; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ESDPATH 73
                                        1 ETDPQTH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ETDPOTH 7
                                                                                                                                                RESULT 12
US-08-947-965-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-947-965-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 71
LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT
                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

```
August 6, 2002, 17:05:16; Search time 66.51 Seconds (without alignments) 13.003 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                   Run on:
```

US-10-020-139-2_COPY_237_245 51 1 DNPQHKTQL 9 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		nucleoprotein - in	nucleoprotein - in	ni - dietororio	,	1			Poprotein -						nacaroprocein III				,	1		,	,	,						1
		B ID		1 VHIV34	1 VHIVXL	1 VHIV68	1 VH1V61	1 VHIVA7	1 VHIVAK	1 VHIVNS	1 VHIV8H	1 VHIVN7	1 VHIVX2	l VHIVX3	1 VHIVX4	1 VHIVX5	1 VHIVX6	6NVIHV 1		1 VHIVN3	l VHIVN2	L VHIVN1	1 VHIVC1	I VHIVM1	l A60028	l VHIVA3	l VHIVA6	l VHIVX1	NHIVN8		2 B36754	A.
	۲.	ch Length DB		2	4	24	4 9	5	4	4.9	49	49	4.9	49	4	5 49	5 49	5 49	5 49	5 49	5 49	49	49	49	498	498	498	498	5 498	498	5 498	498
æP		Score Match	ŀ	7	7	7	7	7	7	7 72	7 72	7 72	7 72	7 72	7 72	7 72	7 72	7 72	7 72	72.	7 72	72	72	72	72	72	72	72	72	72	37 . 72.	7
	Result	No.		٦	2	m	4	ഹ	Q	7	ထ	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

30 37 72.5 498 2 S34418 nucleoprotein - in hypothetical 12.1 32 70.6 104 2 E91124 hypothetical prote 13.1 36 70.6 104 2 E91124 hypothetical prote 13.4 36 70.6 104 2 D97162 hypothetical prote 13.5 70.6 1246 2 D97162 hypothetical prote 13.5 68.6 27.1 2 AG0315 conserved hypothetical prote 13.7 2 AG0315 conserved hypothetical foliation of 12.4 2 AC272 hypothetical prote 12.4 AC272 hypothetical hypothetical prote 12.4 AC272 hypothetical hypothetical prote 12.4 AC272 hypothetical hypothetical hypothetical prote 12.4 AC272 hypothetical hypothetic	RESULT 1 VHIV34 Uncleoprotein - influenza A virus (strain A/PR/8/34) C.Species: influenza A virus (strain 17-Dec-1982 #text_change 24-Feb-1995 R.Morter, G.; Fields, S. Virology 114, 423-428, 1981 A;Title: The structure of the gene encoding the nucleoprotein of human influenza vir A;Reference number: A94327; MUD:82041445 A;Molecule type: genomic RNA A;Residues: 1-498 «MIN> R;Van Rompuy, L.; Min Jou, W.; Huylebroeck, D.; Devos, R.; Fiers, W. Submitted to the Atlas, June 1982 A;Reserence number: A94590 A;Molecule type: genomic RNA A;Residues: 1-346, N', 248-352, 'L', 354-424,' 1', 426-429,' N', 431-498 «VAN> C;Genetics: A;Map position: segment 5 C;Superfamily: influenza virus nucleoprotein	Query Match Best Local Similarity 66.7%; Store 37; DB 1; Length 498; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Oy 1 DNPQHKTQ1 9 1 Db 320 ENPAHKSQL 328 RESULT 2 VHIVX. nucleoprotein - influenza A virus (strain X/Leningrad/54/1 [HIN1]) C; Species: influenza A virus (strain 31-Mar-1993 #text_change 16-Jul-1999 C; Species: influenza A virus (species: influenza A virus (species: influenza A virus (species: influenza A virus (species: influenza A virus C; Species: influenza A virus (species: influenza A virus Signification (species: influenza A virus (
шшшшшшшшш 4 4 4 4 4 4 6 Ош иш 4 8 8 7 8 9 0 0 11 5 11 4 8 8	RESULT VHIV34 NUCLEOPTO C, Date: 1es C, Date: 1es C, Accessin R, Minter, Virolers A, Title: A, Refection R, Van Rome R, Reserime C, Genetic C, Genetic C, Superfam C, Superfam	Query Ma Best Loo Atches Qy 1 Db 320 RESULT 2 VHIVXI nucleoprot C;Species: 3 A;Nete: 31 C;Date: 31 C;Date: 31 C;Date: 31 C;Date: 11 C;Date: 11 A;Netlemis Bioorg. Rh A;Title: S A;Accessio

```
nucleoprotein - influenza A virus (strain A/Udorn/307/72)
C;Species: influenza A virus
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C;Accession: B25612; G36754
R;Buckler-White, A.J.; Murphy, B.R.
Virology 155, 345-355, 1986
A;Title: Nucleotide sequence analysis of the nucleoprotein gene of an avian and a hum A;Reference number: A94345; MUID:87071656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GB.M14922; NID:g325098; PIDN:AAA43686.1; PID:g325099
A.Experimental source: strain A/Udorn/307/72
R.Altmeller, A.; Fitch, W.W.; Scholtissek, C.
J. Cen. Virol. 70, 2111-2119, 1989
A.Title: Blological and genetic evolution of the nucleoprotein gene of human influenz
A.Reference number: A36754; MUID:89361370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 31_Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jul-1999 C;Accession: JN0399; S09650 R;Beklemishev, A.B.; Blynov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; M Bloorg. Khim. 12, 369-374, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Nuclectide sequence of a full-length DNA copy of the influenza virus A/Kiev/A:Reference number: S09650; MUID:86186950
A:Accession: NUG399
A:Molecule type: genomic RNA
A:Molecule type: genomic RNA
A:Residues: 1-498 <BEK>
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X51972; NID:960820; PIDN:CAA36234.1; PID:960821 C;Genetics: A;Gene: NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: segment 5
C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein: phosphoprotein
F:176.345/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                     0;
                                  Score 37; DB 1; Length 498;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoprotein - influenza A virus (strain A/Kiev/59/79 [H1N1])
C;Species: influenza A virus
                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%; Score 37; DB 1;
66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: strain A/Udorn/307/72 [H3N2]
                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: influenza virus nucleoprotein Keywords: nucleoprotein
                               72.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: host Homo sapiens (man)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: segment 5
     Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-498 <ALT>
                                                                                                                                                                       320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-498 <BUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 ENPAHKSQL 328
                                                                                                                                     1 DNPOHKTOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DAPOHKTOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Accession: B25612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Accession: G36754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N'Alternate names: NP protein
C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 08-Apr-1994
C;Accession: D31831
R;Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.
A;Tology 167, 554-567, 1988
A;Title: Identification of sequence changes in the cold-adapted, live attenuated influen
A;Reference number: A31831; MUID:89073759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The sequence of the nucleoprotein gene of human influenza A virus, strain A/NT/
A;Reference number: A04078; MUID:82150233
A;Accession: A04078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Altmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
A:Title: Biological and genetic evolution of the nucleoprotein gene of human influenza
A:Reference number: A36754; MUID:89361370
A;Status: preliminary
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: influenza A virus
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A04078; F3674
R;Huddleston, JA.; Brownlee, G.G.
Nucleic Acids Res. 10, 1029-1038, 1982
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J02137; NID:9324703; PIDN:AAA43465.1; PID:9324704
A;Experimental source: strain A/NT/60/68
A:Map position: segment 5
C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein: phosphoprotein
F:176,345/Binding site: phosphate (Ser) (covalent) *status predicted
                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleoprotein - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])
                                                                                                                                                            Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 498;
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoprotein - influenza A virus (strain A/NT/60/68)
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain A/NT/60/68 [H3N2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: segment 5
C;Superfamily: influenza virus nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: segment 5
C;Superfamily: influenza virus nucleoprotein
C;Keywor&s: nucleoprotein
                                                                                                                                                         Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37;
Pred. No.
                                                                                                                                                         72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.5%;
66.7%;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: genomic RNA A; Residues: 1-498 <HUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: genomic RNA A; Residues: 1-498 <COX>
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-498 <ALT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 ENPAHKSOL 328
                                                                                                                                                                                                                                                               1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: NP
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
```

```
NyAlternate names: NP protein
C:Species: influenza A virus
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C:Accession: C36754
B:Alfmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119; 1989
A:Title: Biological and genetic evolution of the nucleoprotein gene of human influer A:Reference number: A36754; MUID:89361370
A:Residues: 1-498
A:Residues: 1-498
A:Residues: 1-498
A:Cross-references: GB:D00601; NID:9221287; PIDN:BAA00477.1; PID:9221288
                                                                                                                                                                                                                                                                                                              N.Alternate names: NP protein
C.Species: influenza A virus
C.Date: 30.Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C.Accession: G31470
R.Gammellin, M.; Mandler, J.; Scholtissek, C.
R.Gammellin, M.; Mandler, J.; Scholtissek, C.
A.Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A.Reference number: A31470; MUID:89243210
A.Molecule type: genomic RNA
A.Rocession: G31470
A.Molecule type: genomic RNA
A.Rocession: G31470
A.Molecule type: GB:MZ2571; GB:J04339; NID:9325058; PIDN:AAA43668.1; PID:9325059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                    nucleoprotein - influenza A virus (strain A/swine/Hong Kong/6/76 (H3N2))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleoprotein - influenza A virus (strain A/Fort Warren/1/50 [HIN])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleoprotein - influenza A virus (strain A/USSR/90/77 [HIN1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Map position: segment 5
C.Superfamily: influenza virus nucleoprotein
C.Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Superfamily: influenza virus nucleoprotein C.Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: NP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: segment 5
                                                                                      :|| ||:||
320 ENPAHKSQL:328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 ENPAHKSOL 328
                                              1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                       J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
VHIVX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHIVX3
                                                                                                           qq
                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleoprotein - influenza A virus (strain A/Hong Kong/1/68 (H3N2))
C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: S05502
R;Reinhardt, U.; Mandler, J.; Scholtissek, C.
Nucleic Acids Res. 17, 6721, 1989
A;Title: Sequence of the nucleoprotein (NP) gene of the influenza A virus reassortant 81
A;Reference number: S05502
A;Accession: S05502
A;Accession: S05502
A;Molecule type: DNA
A;Residues: 1-498 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Ancession: B.1470
A.Molecule type: genomic RNA
A.Rolecule type: genomic RNA
A.Rolecule type: genomic RNA
A.Rolecule type: genomic RNA
A.Rolecule type: genomic RNA
A.Coss references: Gia.M2577; GB.J04339; NID:y324245; PIDN:AAA43241.1; PID:g324246
A.Coss. references: Gia.M2577; GB.J04339; NID:y324245; PIDN:AAA43241.1; PID:g324246
A.Coss. virol. 70, 2111-2119, 1989
A.Title: Biological and genetic evolution of the nucleoprotein gene of human influenza in A.Reference number: A36754; MUD:89361370
A.Reference number: A36754; MUD
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Wilternate names: Industry A virus (Strain Aynony Nougy)/03 (H3NZ))

C;Species: influenza A virus
C;Species: influenza I (Strain I)
S;Species: influenza A viruses
A;Species: Two subtypes of nucleoproteins (NP) of influenza A viruses.
A;Reference number: A31470; MUID:89243210
A;Reference number: B31470; MUID:89243210
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: EMBL:X15890; NID:g60477; PIDN:CAA33899.1; PID:g60478 C:Genetics:
                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                    nucleoprotein - influenza A virus (strain A/Hong Kong/5/83 (H3N2))
                                   72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 498;
                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 37; DB 1; 66.7%; Pred. No. 19; tive 2; Mismatches
                                                                    Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: segment 5
C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
Query Match
Best Local Similarity 66.77
Berthag 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 6; Conserv
                                                                                                                                                                                                                                  320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ENPAHKSOL 328
                                                                                                                                                                 1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                              QQ
                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
A;Cross-references: GB:U00602; NID:g221289; PIDN:BAA00478.1; PID:g221290
A;Experimental source: strain A/Texas [H3N2]
**Lij. X. S.: Zhoo, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Ne
J. Gen. Virol. 73, 1329-1337, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| ||:||
320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DNPQHKTQL 9
                                                                                                                                                                                                                                                      A:Accession: PQ0423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHIVX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                         A;Title: Biological and genetic evolution of the nucleoprotein gene of human influenza A
A;Reference number: A36754; MUID:89361370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleoprotein - influenza A virus (strain A/Texas [H3N2])
N.Alternate names: NP protein
C.Species: influenza A virus
A.Note: nost Homo Sapiens (man)
C.Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C.Accession: H36754; P00411; P00423
EX.Altmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
A;Title: Blological and genetic evolution of the nucleoprotein gene of human influenza A;Reference number: A36754; MUID: 89361370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Altmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2219, 1989
A;Title: Biological and genetic evolution of the nucleoprotein gene of human influenza
A;Referance number: A36754; MUID:89361370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                    A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 30-Jun-1991 *sequence_revision 30-Jun-1991 *text_change U8-Apr-1994 C;Accession: E36754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoprótein - influenza A virus (strain A/Brazil/11/78 [HIN1])
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 498;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 37; DB 1; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                C, Accession: D36754
R;Altmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
                                                                                                                                                                                                                                                                                                          A.Map position: segment 5
C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: segment 5
C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                    72.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 65.00
Best Local Similarity 65.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: NP protein
C;Species: influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
C; Species: influenza A virus
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-498 <ALT>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||:||
320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-498 <ALT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :1/ ||:||
320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-498 <ALT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DNPQHKTQL 9
                                                                                                                                                                                             A; Accession: D36754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E36754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: H36754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
RAlfmueller, A.; Fitch, W.M.; Scholtissek, C.
J. Gen. Virol. 70, 2111-2119, 1989
A.; Tille: Biological and genetic evolution of the nucleoprotein gene of human influenz
A.; Reference number: A36754; MUID: 89361370
A.; Accession: A36755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: A36755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: NP protein
Cispecies: influenza A virus
Cibate: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
Cibacession: I3470
Ridamellin, M: Mandler, J.: Scholtissek, C.
Wirology 170, 71-80, 1989
A:Title: Two subtypes of nucleoproteins (NP) of influenza A viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1.498 <aLT>
A;Cross-references: GB:D00600; NID:g221285; PIDN:BAA00476.1; PID:g221286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleoprotein · influenza A virus (strain A/swine/Iowa/1976/31 (H1N1))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 19; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 498;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleoprotein · influenza A virus (strain A/California [H1N1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                        A: Experimental source: strain A/Guizhou/54/89 [H3N2]
                                                                                             A;Molecule type: genomic RNA
A;Residues: 23-55 <LIA1>
A:Experimental source: strain A/Hebei/24/89 (H1N2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: influenza virus nucleoprotein
C:Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: segment 5
C:Superfamily: influenza virus nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.58;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: NP protein
C;Species: influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                     A; Molecule type: genomic RNA
A; Residues: 23-55 <LIA2>
                                                                                                                                                                                                                                                                                                                                    A: Map position: segment 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'-hes 6; Conserva
```

```
A; Accession: 131470
A;Molecule type: genomic RNA
A;Rosidues: 1-498 cGAM>
A;Cross-references: GB:M22578; GB:J04339; NID:g325071; PIDN:AAA43676.1; PID:g325072
C;Genetics:
A;Gene : NP
A;Gene : NP
A;Gene in cisegment 5
C;Superfamily: influenza virus nucleoprotein
C;Keywords: nucleoprotein
                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                               Ouery Match 72.5%; Score 37; DB 1; Length 498; Best Local Similarity 66.7%; Pred. No. 19; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     :11 ||:11
Db 320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                       1 DNPQHKTOL 9
                                                                                                                                                                                                                                                                                                                                                            ò
```

Search completed: August 6, 2002, 17:05:17 Job time: 919 sec

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

August 6, 2002, 17:07:36 ; Search time 32.88 Seconds (without alignments) 10.598 Million cell updates/sec

US-10-020-139-2_COPY_237_245 51 1 DNPQHKTQL 9 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	7 in	133 influenz	539 influenza	328 influenza	69 influen	560 influenz	infl		inf		infl.		infl	_	infl			infl		inf	inf		inf	inf	_	_			infl	influen	influen	influen	
		QI .	VNUC_IAANA	VNUC_IAANN	VNUC_IAB37	VNUC_IAB39	VNUC_IABRA	- 1	VNUC_IACAL	VNUC_1ACKG	VNUC_1ACKP	VNUC_1ADAU	VNUC_IADBE	VNUC_IADCZ	VNUC_IADE1	VNUC_IADE2		- 1	VNUC_IADMA	t		- 1	- I	- 1	- 1	VNUC_IAFPR		1	1	1	1	- 1	1	- 1	OFFICE CITY
		Length DB	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	498 1	98	G)	80	98	86	80	86	86	86	86	498 1	86	498 1	498 1	000
ď		Match L	2	2	ς.	ζ.	ζ.	ά.	S.	ζ.	'n.	à	ď	ć,	Ċ.	ď	ς.	ď	~	ď	Α.	Ċ.	ď.	ď.	ď.	oi.	o.	ci.	ď.	ά.	ď	ď.	72.5	ď	c
		Score	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	3.7	37	37	37	7
	Result	No.	н	2	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	La La

VNUC_IAANN STANDARD; PRT; 498 AA. P21433; P80881; 01-MY-1991 (Rel. 18, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Nucleoprotein.

RESULT 2 VNUC_IAANN ID VNUC_IA AC P21433; DT 01-MAY-DT 01-NOV-DT 01-NOV-DE NUCleop

δ

đ	ದ	ದ	۵	æ	ø	ø	ø	ø	ø	ď	Ø
intluenza	influenza	influenza	influenza	influenza	influenza	influenza	influenza	influenza	influenza	influenza	influenza
P26068	P15673	P16979	P22435	P16982	P16980	P15674	P16314	091743	P31609	P15675	P06826
VNUC_IAHJI	VNUC_IAHLO	VNUC_IAHMI	VNUC_IAHO1	VNUC_IAHO2	VNUC_IAHPR	VNUC_IAHTE	VNUC_IAKIE	VNUC_IAKIT	VNUC_IALEN	VNUC_IAMAA	VNUC_IAMAN
_	Г	_	7	-	_	, ,		~	7		г
498	498	498	498	498	498	498	498	498	498	498	498
72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5
37	37	37	37	37	37	37	37	37	37	37	37
			7	38	39	40	41	7	m	4	45

ALIGNMENTS

RESULT 1 VNUC_IANAM STANDARD: PRT: 498 AA. AC P1827: AC P1828: AC
--

```
Wed Aug / 05:46:46 2002
```

between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; 1,07374; AAAS1486.1; -.

this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ö MEDITINE-9323329; PubMed-8474171; Shu L.L., Bean W.J., Webster R.G.; Analysis of the evolution and variation of the human influenza A virus nucleoprotein gene from 1933 to 1990."; J. Virol. 67:2723-2729(1993). NCBI_TaxID=38951, 38952, 73485, 38961, 38962, 38969, 11441, 38978; MEDLINE=89073759; PubMed-2974219; MEDLINE=89073759; PubMed-2974219; Cox N.J., Kitame F., Kendal A.P., Maassab H.F., Naeve C.; Cox H.J., Kitame F., Requence Changes in the cold-adapted, live attenuated influence vaccine strain, A/Ann Arbor/6/60 (H2N2)."; .. VARIANT 23 23 N -> T (IN COLD-ADAPTED ISOLATE). VARIANT 34 34 G -> D (IN COLD-ADAPTED ISOLATE). SEQUENCE 498 AA; 55963 MW; E51D08494E9FA075 CRC64; 72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3; ative 2; Mismatches 1; Indels Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Viruses; ssRNA negalive-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus. Virology 167.554-567(1988). Influenza A virus (strain A/Beijing/337/89), Influenza A virus (strain A/Beijing/352/89), Influenza A virus (strain A/Beijing/35/89), Influenza A virus (strain A/Guangdong/38/89), Influenza A virus (strain A/Guangdong/9/87), Influenza A virus (strain A/Memphis/8/88), Influenza A virus (strain A/Memphis/8/88), Influenza A virus (strain A/Memphis/8/88), OUTS 29 008029; PRT; 498 AA. 007539; 008029; O1FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) O1-FEB-1995 (Rel. 31, Last annotation update) Influenza A virus (strain A/Ann Arbor/6/60). PIR; D31831; VHIV61. InterPro; IPR002141; Flu_NP. EMBL; M23976; AAA43451.1; -. Best Local Similarity 66.79 Matches 6; Conservative Pfam; PF00506; Flu_NP; 1. Influenza A virus. SEQUENCE FROM N.A. 320 ENPAHKSOL 328 NCBI_TaxID=135322; SEQUENCE FROM N.A. 1 DNPQHKTQL 9 Nucleoprotein. Nucleoprotein Query Match VNUC_IAB37 Matches

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9233239; PubMed-8474171; Shu L.L., Bean W.J., Webster R.G.; Shu L.L., Bean W.J., Webster R.G.; Analysis of the evolution and variation of the human influenza virus nucleoprotein gene from 1933 to 1990."; J. Virol. 67:2723-2729(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Pest Local Similarity 66.7%; Pred. No. 8.3;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                            72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Influenza A virus (strain A/Beijing/39/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 AA; 56180 MW; C4C61E024F1AA2C1 CRC64;
                                                                                                                                                                                                                                                                               498 AA; 56224 MW; 28F46CA5BBD1DAC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                    EMBL, L07373, AAA51490.15
EMBL, L07373, AAA51489.17
EMBL, 107370, AAA5148.17
EMBL, L07370, AAA51494.17
EMBL, L07372, AAA5141.17
EMBL, L07372, AAA51483.17
EMBL, 107354; AAA51483.17
InterPro; IPR002141; Flu_NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L07358; AAA51485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60...
Est Local 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                    Pfam; PF00506; Flu_NP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID~38955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleoprotein.
                                                                                                                                                                                                                                                                       Nucleoprotein
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNUC_IAB39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                008028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

1 DNPQHKTQL 9

ò

This SWISS-PROT entry is copyright. It is produced through a collaboration

-! - FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.

```
VNUC_IACAL
P18070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                            VNUC_TACAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                      δ
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                               Altmueller A., Fitch W.M., Scholtissek C.; "Biological and genetic evolution of the nucleoprotein gene of human" \mbox{\tt Biological}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90204657; PubMed-2319644;
Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.;
"Evolution of the nucleoprotein gene of influenza A virus.";
J. Virol. 64:1487-1497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.5%; Score 37; DB 1; Length 498; Best Local Similarity 66.7%; Pred. No. 8.3; Matches 6; Couservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                  J. Gen. Virol. 70:2111-2119(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498 AA; 55988 MW; 4B09757425A7F8DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Budgerigar/Hokkaido/1/77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                     Influenza A virus (strain A/Brazil/11/78).
                                                                                                                                                                                                                                      MEDLINE=89361370; PubMed=2769232;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D00599; BAA00475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; E36754; VHIVX4.
Interpro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                      STANDARD;
                                                                                                                                                                                                                                                                        influenza A viruses.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
  320 ENPAHKSQL 328
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=150159;
                                                                                                                                                                                                     NCB1_TaxID=11331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleoprotein.
                                                                                                                                 Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNUC_IABUD
P15660;
                                                                     VNUC_IABRA
P18069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                         RESULT 6
VNUC_IABUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qa
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altmueller A., Fitch W.M., Scholtissek C.; "Biological and genetic evolution of the nucleoprotein gene of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Gen. Virol., 70:2111-2119(1989).
-i- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             498 AA; 56291 MW; 43990247E22774EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 AA; 56283 MW; FAD26B1023B30894 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%; Score 37; DB 1; 66.7%; Pred. No. 8.3; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/California/10/78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89361370; PubMed=2769232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D00600; BAA00476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A36755; VHIVX6.
InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                           Flu_NP.
                                                                                                                                                                                                                                                                            EMBL; M30765; AAA43486.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                           InterPro; IPR002141; Flu_
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    influenza A viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DNPOHKTOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                 Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleoprotein
```

```
qq
                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                        Reinhardt U., Scholtissek C.: "Comparison of the nucleoprotein genes of a chicken and a mink "Comparison of the nucleoprotein genes of a chicken and a mink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90204657; PubMed=2319644; MEDLINE=90204657; PubMed=2319644; Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.; Gorman O.T., Bean W.J., Kawaoka Y., Webster R.G.; Evolution of the nucleoprotein gene of influenza A virus."; J. Virol. 64:1487-1497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Chicken/Pennsylvania/1/83).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                 Arch, Virol, 103:139-145(1988).
-!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA; 56235 MW; ECEEADC066E72FE9 CRC64;
                                                                                                                           Influenza A virus (strain A/Chicken/Germany/n/49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                        498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                         PRT;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-89104698; Pubmed-3214270;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M24453; AAA43470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A43494; VHIVC1.
InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66...
Fre 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                         STANDARD;
                                                                                                                                                                                                                                                                     influenza A H 10 virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| ||:||
320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza A virus.
NCBI_TaxID=11341;
                                                                                                                                                                                  NCBI_TaxID=11339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleoprotein.
                                                                                                   Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNUC_IACKP
P15661;
                           VNUC_IACKG
P16984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
RESULT 8
VNUC_IACKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNUC_IACKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its much by non-profit institutions as long as its content is in no way much ited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               0
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-91251223: PubMed*2041090;
Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y.,
Webster R.G.
"Evolution of influenza A virus nucleoprotein genes: implications for the origins of HINI human and classical swine viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
O
                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (strain A/Duck/Australia/749/80).
Viruses: ssRNA negative-strand viruses: Orthomyxoviridae:
Influenza virus A and B group: Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Virol. 65:3704-3714(1991).
-!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 AA; 56221 MW; BC4F1473C231C813 CRC64;
                                                                                                                                                                                                                  498 AA; 56274 MW; BFD13C3A68DB4BAB CRC64;
                                                                                                                                                                                                                                                                                  Score 37; DB 1;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 AA.
                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKT;
                                                                                                                                                                                                                                                                                     72.58;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M63783; AAA52244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                            InterPro; IPR002141; Flu_NP. Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7v
6, Conservative
                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 66./*
Free 6; Conservative
                                                                                                                         EMBL; M30768; AAA43489.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleoprotein.
                                                                                                                                                                                              Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
VNUC_IADBE
ID VNUC_IADBE
AC P26064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNUC_1ADAU
P26065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNUC_IADAU
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its model by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                       MEDINE-91251233; Pubmed-2041090; Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y., Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y., Webster R.G.; Bean W.J., Kawaoka Y., Donatelli J., Guo Y., Evolution of influenza A virus nucleoprotein genes: implications for the origins of HNN human and classical swine viruses."; J. Virol. 65:3704-3714(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MADDINE-9120464; MEDILINE-90204657; PubMed-2319644; GOTHME-907-07., Bean W.J., Kawaoka Y., Webster R.G.; "FVOLUTION of the nucleoprotein gene of influenza A virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                  Viruses; ssRNA negative-strand viruses; Orthomysoviridue;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 64:1487-1497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 AA; 56253 MW; 49B657952426CEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Duck/Czechoslovakia/56).
                                                                        Influenza A virus (strain A/Duck/Beijing/1/78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
 01-WAY-1992 (Rel. 22, Created)
01-WAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002141; Flu_NP. Pfam; PF00506; Flu_NP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M63782; AAA52243.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 ENPAHKSQ1, 328
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11353;
                                                                                                                                 NCBI_TaxID=11352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleoprotein.
                                               Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNUC_IADCZ
P15662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNUC_IADC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolution of influenza A virus nucleoprotein genes: implications for the origins of HINI human and classical swine viruses."; J. virol. 65:3704-3714(1991),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Orthomysoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEĎLINE-91251223; PubMed-2041090;
Gorman O.T., Bean W.J., Kawacka Y., Donatelli I., Guo Y.,
Webster R.G.;
                                                                                                                                                                      72.5%; Score 37; DB 1; Length 498 66.7%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 AA; 56305 MW; 5579A6F6DA1934A5 CRC64;
                                                                                                498 AA; 56244 MW; D393CD14859491ED CRU64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Duck/England/1/56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8.3;
2; Mismatches
                                                                                                                                                                                              Pred. No. 8.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002141; Flu_NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M63780; AAA52241.1; -.
                     InterPro; IPR002141; Flu_NP. Pfam; PF00506; Flu_NP; 1.
EMBL; M30762; AAA43483.1; -
                                                                                                                                                 Query Match
Best Local Similarity 60.7.
Loca 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                               320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                            1 DNPQHKTQI, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleoprotein.
                                                                           Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                VNUC_TADE1
P26062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNUC_IADE2
P26063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                      SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNUC_IADE2
                                                                                                                                                                                                                                                                                                                                                                                                                             VNUC_IADE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license eightenent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license lises agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                          'Evolution of influenza A virus nucleoprotein genes: implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammelin M., Mandler J., Scholtissek C.;
"Two subtypes of nucleoproteins (NP) of influenza A viruses.";
Virology 170:71-80(1989).
-i- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.5%; Score 37; DB 1; Length 498; 66.7%; Pred. No. 8.3; 1; Indels Live 2; Mismatches 1; Indels
            Influenza A virus (strain A/Duck/England/1/62).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                      the origins of H1N1 human and classical swine viruses.";
J. Virol. 65:3704-3714(1991).
-!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91251223; PubMed-2041090;
Gorman O.T., Bean W.J., Kawaoka Y., Donatelli I., Guo Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 AA; 56328 MW; 5F0EA230D13C31C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Duck/Hong Kong/7/75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89243210; Pubmed~2718389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22573; AAA43097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B31470; VHIVN2.
InterPro; IPR002141; Flu_NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flu_NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M63781; AAA52242.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.77
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ENPAHKSOL 328
                                                                        Influenza A virus.
NCBI_TaxID=11355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleoprotein
                                                                                                                                                                                         Webster R.G.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNUC_IADHK
P16978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNUC_IADHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
DR PFam; PF00506; Flu_NP; 1.

KW Nucleoprotein.

SQ SEQUENCE 498 AA; 56239 MW; 9C37ACC466647C7D CRC64;

Query Match

Best Local Similarity 66.78; Score 37; DB 1; Length 498;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps

Qy 1 ENPOHRTOL 9

:|| || || || || ||

Db 320 ENPAHKSQL 328

Search completed: August 6, 2002, 17:07:36
```

influenza influenza influenza influenza influenza influenza

influenza influenza

uenza influenza influenza influenza

infl

0911D4 0911D3 0911D2 0911D1 0911D0

influenza influenza

0911E8 0911E7 0911E5 0911E5 0911E2 0911E1 0911E0 0911D9 0911D9

influenza

```
Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     237 DNPQHKTQL 245
1 DNPQHKTQL 9
                                                                                                                                                                                                                                                      NCBI_Tax LD=9606;
                                                                                                                                                                                                                                                                      Tracey A.;
                                                                                                                                                                                                                                 BA49G10.1.
096DR5;
                                                                                                                                                                                                      Q9BQQ0;
                                                                                                                                                                                                09B000
                                                                                                                                                                                                                                                                                                                                                               Q96DR5
                                                                                                                                                                                                                                                                                                                                                      7
RESULT
                                                                                                                                                                                          09B000
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                          Q96DR5
                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                              influenza a
influenza a
influenza a
                                                                                                                                                                                                                                                                                                                                              influenza a influenza a influenza a influenza a influenza a influenza a
                                                                                                                                                                                                                                                                                                                                                                          influenza a
influenza a
                                                                                                                                                                                                                                                                                                                                                                                          influenza a
influenza a
                                                                                                                                                                                                                                                                                                                                                                                     influenza a
                                          (without alignments)
13.983 Million cell updates/sec
                                                                                                                                                                                                                                                                                                               09bqq0 homo sapien
096dr5 homo sapien
007163 mycoplasma
                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                     August 6, 2002, 17:09:32; Search time 111.35 Seconds
                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                    091193
091192
091190
091190
091167
091167
091163
091163
                                                                                                                                                                                                                                                                                                                                Q91u38
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                               562222 seqs, 172994929 residues
                                                     US-10-020-139-2_COPY_237_245
51
                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                        007163
091U38
091UG3
091IG3
091IF0
091IF7
091IF7
091IF7
                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                              Q9BQQ0
Q96DR5
                                                                                                                                                                                                                               sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                               sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                               sp_bacteriap:*
                                                                                                                                                                                                    sp_organelle:*
                                                                                                                                                               sp_archea:*
sp_bacteria:*
                                                                                                                         length: 2000000000
                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                     sp_archeap:*
                                                                                                                                                                                                                                         sp_rvirus:*
                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                         sp_plant:*
                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                          sp_mammal:*
                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                         SPTREMBL_19:*
                                                                                                                                                                          sp_fung1:*
                                                                                                                                                                                                          sp_phage: *
                                                                     1 DNFQHKTQL 9
                                                                                                                                                                                               sp_mhc:*
                                                                                BLOSUM62
                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 20
                                                                                                                                                                                                                                                                                                              4.0.0 / 8.0.
                                                                                                                                                                                                                                                                                                    Score
                                                                Perfect score:
                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                               Database :
                                                                     Sednence:
                                                                                                Searched:
                                     Run on:
```

```
0
                                                                                                                                                                                                                                                                                                     influenza
                                                                                                                                                                                                                                                                                                                     influenza
                                                                                                                                                                                                                                                                                                                                   influenza
                                                                                                                                                                                                                                                                                                                                                  influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
0911168
0911167
0911167
0911167
0911167
0911167
0911167
0911167
0911168
0911168
0911169
0911169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 4; Length 249; 100.0%; Pred. No. 0.03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2001) to the EMBL/GenBank/UDBJ databases.
EMBL: AL121901; CAC03546.1; --
SEQUENCE 249 AA; 27011 MW; E64E0794A1B4DB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49610.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
PAROTID.SECRETORY PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                  0911C8
0911C7
0911C6
0911C5
0911C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC AC DT DT DT DT OS
```

Result Š. ö

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=132728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| ||:||
58 ENPAHKSQL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 ENPAHKSQL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q911G2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q911G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0911G3
          RAT RET DE L'AL DE L'A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARP ARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y., Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
                                                                                                                                                                                         Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the FSP/plunc family of BPT proteins is expressed in the human parotid gland.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF432917: AA128113.1;
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=155225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Caps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Moillicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 4; Length 249; 100.0%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.5%; Score 39; DB 2; Length 252; 87.5%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ben Abdelmoumen B., Roy R.S., Brousseau R.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 252 AA; 27323 MW; 262E4302C6BE5226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLEEL 04, Created)
01-JUL-1997 (TrEMBLEEL 04, Last sequence update)
01-JUL-1997 (TrEMBLEEL 04, Last annotation update)
PCL42-56 IMMUNODOMINANT MEMBRANE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (A/Hong Kong/507/97(H5N1)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOCAPSID PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U66315; AAB58471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAİM=A/HONG KONG/507/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma synoviae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111111
237 DNPQHKTQL 245
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 NPQHKTYL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=WVU 1853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2109;
                                                                                                                                                              TISSUE-PAROTID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               007163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            007163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  091038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
1007163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
   ò
```

```
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=132729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                           Gaps
Subbarao K.;
"Avian influenza A HSN1 and H9N2 viruses bearing a specific constellation of nonglycoprotein genes caused illness in humans.";
Submitted (APR-2000) to the EMBL/GenBank/NDBJ databases.
EMBL; AF255763; AAK49289.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINF-20347342; PubMed-10888619; Ocetho J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A., Osterhaus A.D., Rimmelzwaan G.F., "Antigenic drift in the influenza A virus (H3N2) nucleoprotein and secape from recognition by cytotoxic T lymphocytes."; J. Virol. 74:6800-6807(2000).
                                                                                                                                                                                                                                                                                                                                                        ć
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                           72.5%; Score 37; DB 12; Length 121; 66.7%; Pred, No. 8.4; 1; Indels vative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.5%; Score 37; DB 12; Length 152; Best Local Similarity 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; indels
                                                                                                                                                  152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Influenza A virus (A/Netherlands/001/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza A virus (A/Netherlands/002/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20347342; Pubmed=10888619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF225709; AAF87330.1;
InterPro; IPR002141; Flu_NP.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00506; Flu_NP; 1.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
```

ö

```
0;
                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (A/Netherlands/007/94 (H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132730;
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A., Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225710; AAF87331.1:
PinterPro: IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP: 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-20347342; PubMed-10886619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.,
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL, AF25711; AAF87332.1;
InterPro; IPR002141; Flu.NP.
Pfan.
NON_TER
                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.5%; Score 37; UB 12; Length 152; 66.7%; Pred. No. 11; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                      72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                      16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROPEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (A/Netherlands/006/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA.
                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                       152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conservat
                                                                                                                                                     152 1
152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 1
152 AA;
                                                                                                                                                                                                                                                                                                           81 ENPAHKSOL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 ENPAHKSOL 89
                                                                                                                                                                                                                                                                                        1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Q911G1
Q911G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                091160
                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091160
                                                                                                                                                                                                                                                                                                                                                                                          Q911G1
                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (A/Netherlands/008/94 (H3N2)).
Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                 SEQUENCE FROM N.A.

WEDLINE-20437432, PubMed-10888619;
Wooten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-20347342; Pubmed-1088619;
MEDLINE-20347342: Pubmed-1088619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
Scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225713; AAF87334.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.5%; Score 37; DB 12; Length 152; Best Local Similarity 66.7%; Pred. No. 11; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       152 152
152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (A/Netherlands/017/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                             J. Virol. 74:6800-000/......
BRBL, ARE25733.1; -.
InterPro: FPR002141; F10_NP.
Pfam; PF00506; F10_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 72.5 Best Local Similarity 66.7 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=132732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ENPAHKSOL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ENPAHKSOL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q911F9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9IIF8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q911F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
Q911F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9IIF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ON DATE OF THE ORDER OF THE ORD
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
```

```
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                        Influenza A virus (A/Netherlands/020/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 152 AA
                                                                                                                                                                                                                                                                                                        Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20347342; Pubmed-10888619;
                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity bo...
6, Conservative
                                                                                                                                                                                                             Pfam; PF00506; Flu_NP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 ENPAHKSQL 89
                                                                                                                                                                                                                                                                                                                                                                         81 ENPAHKSQL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DNPOHKTOL 9
                                                                                                                                                                                                                                                                                                                                                1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q911F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q911F5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9IIF4
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q911F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9IIF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID
AC
                                                                                                                                                                                                                                                                                                                                                                           q
 ..
O
                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Caps
                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-203473472; PubMed=10888619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
Antigonic drift. in the influenza A virus (H3N2) nucleoprotein and
escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL: AR225715; AAF87336.1:
InterPro; IPR002141; Flu_NP.
Ffam: PF00566; Flu_NP.
NON_TER
                                                           MEDITRE-20147342; PubMed-10888619; Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchler R.A., Osterhaus A.D., Rimmelzwaan G.F.; "Antigenic drift in the influenza A virus (H3N2) nucleoprotein and escape from recognition by cytotoxic T lymphocytes."; J. Virol. 74:6800-6807(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.5%; Score 37; DB 12; Length 152; Best Local Similarity 66.7%; Pred. No. 11; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                     72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                 SECUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza A virus (A/Netherlands/018/94 (H3N2)).
                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                              EMBL; AF225714; AAF87335 1; -. Interpro; IPR002141; F10_NP. Pfam; PF00506; F10_NP; 1. NON TER
                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=132734;
                         NCBI_TaxID=132733;
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| ||:||
81 ENPAHKSQL 89
                                                                                                                                                                                                                                                                                                                          :|| ||:||
81 ENPAHKSOL 89
                                                                                                                                                                                                                                                                                                           1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DNPQHKTQL 9
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091156;
                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IIF6
                                                                                                                                                                                                                                                                                                                                                                                                     0911F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
Q9IIF6
                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA PA PA
                                                                                                                                                                                                                                                                                                            ô
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (A/Netherlands/021/94 (H3N2)).
Viruses; ssRwa negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_Tax10-132736;
Viruses; ssRNA negative-strand viruses; Orthomysoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID-132735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vosten J.T., Bestebrocr T.M., Nieuwkoop N.J., Fouchier R.A., Sostefaus A.D., Rimmelzwaar G.F.;
"Antigenic drift in the Influenza A virus (H3N2) nucleoprotein and escape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL; AF225717: AAF87338.1;
InterPro: IPR02141; Flu_NP.
Pfan; PF00506; Flu_NP: 1.
NON_TER.
                                                                                                                                                                           MEDLINE=20347342; PubMed-10888619; Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier K.A., Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier K.A., Voeten J.T., Raimelzwaan G.F.; Affile Sacher Grift in the influence A virus (H3N2) nucleoprotein and escape from recognition by cyloloxic T lymphocytes."; J. Virol. 74:6806.06807(2000).

EMBL; AF225716; AAF87337.1; -
InterPro; IPR002141; Flu_NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 152 152
NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132738;
                                                                                       Influenza A virus (A/Netherlands/022/94 (H3N2)).
Viruses; ssRNA negative-strand viruses, Orthomyxxviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=132737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WEDLINE-20347347.3.

VOETEN J.T. Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,

Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,

Osterhaus A.D., Rimmelzwaan G.F.,

"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and

scape from recognition by cytotoxic T lymphocytes.";

J. Virol. 74:6800-6807(2000).

EMBL, AF225718; AAF87339.1;

InterPro; FR002141; Flu_NP.

Pfam, PF00506; Flu_NP:

NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WEDLIKE=20347342. Pubmed=10888619;
Voeten J.T., Bestebroer T.M., Nieuwkoop N.J., Fouchier R.A.,
Osterhaus A.D., Rimmelzwaan G.F.;
"Antigenic drift in the influenza A virus (H3N2) nucleoprotein and
scape from recognition by cytotoxic T lymphocytes.";
J. Virol. 74:6800-6807(2000).
EMBL: AF225719; AAF87340.1;
InterPro; IPR002141; Flu_NP.
Pfam; PF00506; Flu_NP:
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.5%; Score 37; DB 12: Length 152; Best Local Similarity 66.7%; Pred. No. 11; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.5%; Score 37; DB 12; Length 152; 66.7%; Pred. No. 11; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                               NON_TER 152 152
SEQUENCE 152 AA; 16846 MW; F9F9594CE8F2D01A CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-027-2000 (TrEMBLrel. 15, Created)
01-027-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (A/Netherlands/026/94 (H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| || || || 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0911F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9IIF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9IIF3
ID Q9
```

ô

0; Gaps

:|| ||:|| 81 ENPAHKSQL 89

1 DNPQHKTQL 9

ò

```
Search completed: August 6, 2002, 17:09:32 Job time: 934 sec
```

Run on:

MO

binding/translo coli proliferat Amino acid sequenc Drosophila melanog Equine influenza v Equine influenza v Equine influenza v Equine influenza v Human ORFX ORF933 Drosophila melanog Novel human diagno

Escherichia coli p Propionibacterium

```
Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                  AAW41166
AAY38750
AAY38751
                                                                                                                AAB41169
ABB69159
                                                                       AAE09058
                                                                                                                                     AAR38309
                                                                                                                                                ABG12679
                                                                                                                                                                                                                                  AAY38748
                                                                                                                                                                                                                                                                                   AAG81272
                                                                                                                                                                                                                                                                                                                   AAR25068
                                                                                                                                                                                                                                                                                                                             ABB23036
                                                                                                                                                                                                                                           AAY08963
                                                                                                                                                                                                                                                     AAB95761
                                                                                                                                                                                                                                                                          AAY50820
                                                                                                                                                                                                                                                                                                                                        AAW38522
                                                                                           AAE09057
                                                                                                                                                                                                                                                                                                         ABB62601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature hPSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69221 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                AAY51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human parotid secretory protein.
  97WO-US23522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0034429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19..249
                                                                                                                                     412
1063
63
87
306
345
362
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; diagnosis.
WO9828420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998.
 AAW69221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW69221
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine influenza v
Equine influenza v
SIV strain H1N1 nu
SIV strain H3N2 nu
SWinepox virus Hin
                                                                                                                                                                                                                                                                                                            2: SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
2: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
3: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
3: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
5: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
6: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1984.DAT:*
7: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:*
8: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
9: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
10: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
11: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
12: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
13: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
14: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
15: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
16: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
17: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parotid secr
Human parotid secr
Human PRO1025 prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted pro
Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein segu
                                                                  August 6, 2002, 16:52:54; Search time 138.55 Seconds (Without alignments) 7.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     747574 seqs, 111073796 residues
                                                                                                    US-10-020-139-2_COPY_237_245
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW60682
AAB24069
AAB25765
AAB75351
AAB75351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW69221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09054
                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                     A_Geneseq_032802:*
                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
19
19
19
19
19
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
100.0
72.5
72.5
72.5
72.5
72.5
                                                                                                                                                                                                                                Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                          Perfect score:
                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
37
37
37
                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                       Searched:
                                                                                                                                     Sequence:
```

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM;

Duan R,

AAE09053 AAW68409 AAW68407 AAW55986

28 4 8 9 7 8 9 1 1 1 1 1 1 1 1

Result õ

A. gossypii ORF 2 Human protein sequ S. tendae nicomyci Streptomyces tende Human AFP protein

Drosophila melanog hLIF-R. Homo sapi hLIF-R. Homo sapi Protein #5035 enco S. pneumoniae gruustreptococcus pneu

Drosophila melanoq

Arabidopsis thalia Arabidopsis thalia

Sequence of the P4

Propionibacterium Propionibacterium Metal-regulated tr

Neisseria gonorrho Neisseria gonorrho Neisseria meningit

gastrointestinal tissues

```
..
O
                                                                                                                                                                                      isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hESP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immuno edfensive, endocrine or immuno system disorders. A particular application or immuno system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and application is diagnosis of cancers of the salivary gland, thymus and agence and may be expressed in vivo from the DNA. The protein is expressing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, thereby, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secretory tissue; gastrointestinal tissue; HPSP, Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or
                                                                                                                                                           This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and
                                               New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parotid secretory protein; human; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 19; Length 249; 100.0%; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW60682 standard; Protein; 249 AA.
                                                                                                                         Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0749288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US20651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overy Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hPSP-binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandman O, Goli SK;
WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 dnpqhktql 245
                 N-PSDB; AAV44759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB, AAV37699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9821329-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07 - NOV - 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW60682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAW60682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
that bind specifically to, and modulate activity of HPSP). Antaqonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune discases particularly or secretory or gastrointestinal tissue, e.g. cancer of salivary giand, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, claves disease, thyroiditis, insulin-dependent diabetes; pancreatitis, cortaining expression vectors comprising the HPSP nucleic acid are used to roduce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective: antiinflammatory; immunosuppressive; immunostlmulant; antiangiogenic; leukaemia; lymphoid malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal disorder; glial disorder; astrocytal disorder; angiogénic; pypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammalory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 51; DB 19; Length 249; 100.0%; Pred. No. 0.091; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24069 standard; Protein; 249 AA.
Claim 1; Fig 1A-C; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US12252.
99US-0141037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0145698.
99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0143048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JAN-2000; 2000WO-US00376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-2000; 2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi AJ, Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 dnpqhktql 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200053755-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-1999;
26-JUL-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

99US-0141032

```
25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
   The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO6199, PRO199, PRO810, PRO6194, PRO190, PRO1090, PRO1019, PRO1050, PRO1030, PRO1097, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO2198, PRO2199, PRO834, PRO1317, PRO1151, PRO2199, PRO2199, PRO2199, PRO834, PRO1317, PRO1110, PRO2199, PRO2199, PRO2199, PRO8191, PRO101917, PRO1111, PRO1151, PRO1161, LUMOUR Cell growth. The PRO POLIPHETICS can be used to inhibit tumour cell treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                              those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
                                                                                                                                                                                                                                                                                                                                      colorectal, prostate, pancratic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemias and lymphoid maliganches, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC$8242 to AAC$836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC$8357 to AAC$8357 to AAC$84089 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                       Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 21; Length 249; 100.0%; Pred. No. 0.091; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein SEQ 1D #77.
                                                                                                                  Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Some Best Local Similarity 100.0%; Promatches 9; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0113686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
Watanabe CK, Wood WI;
                            WPI; 2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 dnpghktgl 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DNPQHKTOL 9
                                            N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200037491-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
```

```
therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA8725-A8774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequences, and a purified antibody capable of binding to one of the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The CDNAS may also be useful in diagnostic, forensic, gene
                                                                                                                                                                                                                                                        Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 21; Length 249; 100.0%; Pred, No. 0.091; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; prevention; treatment; diagnosis; disease;
                                                                   Bougueleret L, Dumas J, Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0141032.
99US-0469099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                          WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                   mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 dnpghktql 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DNPOHKTOL 9
                                                                                                                                                                             N-PSUB; AAA87727
(GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200100806-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

```
Claim 5; Page 166-167; 172pp; English.
          Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09054;
                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09054
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                              antibilizamentory, antirhementory antiarthritic; immunosuppressive, antibilizamentory antirhementory antiarthritic; immunosuppressive, antibacterial; endocrine; cardiant; central nervous system; virucide; antiagragant; haemostatic; vulnerary; antialcer; costeopathic; eacemais, dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antialdepressant; nootropic; antiparkinsonian; infection; antianaphylactic; rheumatoid arthritis; septic shock; panorealtis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopolelic disorder; platelet disorder; asthma: thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabotes; multiple sclerosis; depression;
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection \cdot
                                                                                                       The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with
                                             49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                      100.0%; Score 51; DB 22; Length 249; 100.0%; Pred. No. 0.091;
                                                                                                                                                                                                                              0; Indels
Jobert S;
                                                                                                                                                                                                                              0; Mismatches
Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:1260.
                                                                                Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                          AAM25745 standard; Protein; 260 AA.
                                                                                                                                             inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (first entry)
                                                                                                                                                                                          Query Match
Best Local Similarity TUV...
9, Conservative
Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-457603/49.
                      WPI; 2001-071487/08.
                                                                                                                                                                                                                                                                             237 dnpqhktql 245
                                                                                                                                                                   249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                      1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                     Sequence.
                                                                                                                                                                                                                                                                                                                                                                AAM25745;
                                                                                                                                                                                                                                                                                                                  Θ
                                                                                                                                                                                                                                                                             qq
```

```
AM2593. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinitianmatory; antinitheumatic; antiartheits; they are expressed in, such as: antinitianmatory; antiartheumatic; antiartheits; they are expressive antiabatterial; endocrine; cardiant; cardiant; cardianesmic; antianeamic; antianeamic; antianeamic; antianeamic; antianeamic; antianeamic; antianeamic; cardianeamic; cardianeamic; cardianeamic; cardianeamic; of antiabetic; cytostatic; neuroprotective; antideptessant; nootropic; antidabetic; cytostatic; neuroprotective; antideptessant; nootropic; contidabetic; cytostatic; neuroprotectides are useful for screening for approtein and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rehumatoid arthritis, septic shock, pancreaticis, cardiac dysfunction, infections, autolumnuity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, contended influent immunodeficiency, eczema, allergic rintitits, asthma, diabetes, cancer, multiple sclerosis, depression, antended and antended influence, multiple sclerosis, depression, antended and d antended andended 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equine influenza virus; el: cold adaptation; temperature sensitivity; vaccine; neiwtlNP-C-656 DNA; PeiwtlNP-C-217 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 22; Length 260; 100.0%; Pred. No. 0.095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equine influenza virus H3N8 PeiwtlNP-C-217 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE09054 standard; Protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2001; 2001WO-US05048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000; 2000US-0506286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine influenza virus H3NB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100. Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Youngher JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-522584/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 dnpghktgl 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD15725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200160849-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dowling PW,
```

Ŋ

;;

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equine influenza virus; ei; cold adaptation; temperature sensitivity; vaccine; neiwtlNP-C-679 DNA; PeiwtlNP-C-225 protein.
                                                                                                                                                                                                                                                                                                    Gaps
     The patent discloses coid-adapted equine influenza viruses and reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is equine influenza (ei) virus hans beintl (whild type) NP-C-217 protein which is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as
                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses cold-adapted equine influenza viruses and
                                                                                                                                                                                                                                                            72.5%: Score 37: DB 22; Length 217; 66.7%: Pred. No. 34; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine influenza virus H3N8 PeiwtlNP-C-225 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key Location/Qualifiers
Misc-difference 217..218
Misc-difference 224..225
Misc-difference 224..225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 165-166; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by CT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE09053 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2000; 2000US-0506286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001; 2001WO-US05048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine influenza virus H3N8
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66...
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Youngner JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-522584/57.
                                                                                                                                                                                neiwtlNP-C-656 DNA.
                                                                                                                                                                                                                    217 'AA;
                                                                                                                                                                                                                                                                                                                                                                        39 enpahksql 47
                                                                                                                                                                                                                                                                                                                                     1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD15724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200160849-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dowling PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections
                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE09053;
                                                                                                                                                                                                                                                                                                                                                                                                                           Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE09053
```

```
digestive disease; Aljeszky's disease virus; pseudorables virus; vaccine; suid herpesvirus 1; swine influenza virus; hog cholera virus; vector; porcine respiratory and reproductive syndrome virus; nucleoprotein; SIRSV: swine infertility and respiratory syndrome virus; nucleoprotein; Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV; HCV:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from Anjeskyl's disease virus, swine influence virus (SIV), portine respiratory and reproductive syndrome virus (PRRSV), hog cholera virus (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. This sequence represents the SIV strain HINI nucleoprotein. The coding sequence was subcloned into the plasmid pVRIO12 to generate plasmid pPB142 for use in the vaccine.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multi-valent polynucleotide varcines against porcine pathogens - consist of at least 3 plasmids able to express protective antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a multivalent vaccine for protecting pigs
cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is equine influenza (ei) virus neiwtlnP-C-679 DNA.
                                                                                                                                                                                                                            .;
O
                                                                                                                                                                                       72.5%; Score 37; DB 22; Length 225;
66.7%; Pred. No. 35;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 19; Length 498;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                AAW68409 standard; Protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Fig 8; 63pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIV strain HlN1 nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.58;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96FR-0009338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96FR-0009338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999 (first entry)
                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from specified viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swine influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WP1; 1998-112824/11.
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                     225 AA;
                                                                                                                                                                                                                                                                                                       39 enpahksgl 47
                                                                                                                                                                                                                                                                    1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV49295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2751224 - A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW68409;
                                                                                                                                         Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                AAW68409
                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8×868888×8
                                                                                                                                                                                                                                                                      ò
```

Page

Matches

AAW68407

```
The present sequence represents a protein from a Swinepox virus strain

Kasza isolate S-SPV-001 HindIII M fragment DNA fragment, which is used in
an example from the present invention. The present invention specifically
describes recombinant swinepox virus (SPV) comprising a foreign DNA (I)
inserted into a SPV genome which is capable of being expressed in a host
cell into Which the virus is introduced, where (I) is inserted into: (a)
an ECORI site within a region corresponding to a 3.2 kb subfragment of
the HindIII K fragment which contains both a HindIII and an ECORI site,
of the SPV genome, and optionally (b) an AccI site within a region
corresponding to a 3.6 kb HindIII to Bgl11 subfragment of the HindIII M
fragment. The recombinant SPV can be used in a vaccine for immunising an
animal against SPV. The invention also provides a method for testing a
corresponding particularly containing S-SPV-008, or is infected with the
vaccine, particularly containing S-SPV-008, or is infected with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant SPV can be used in a diagnostic assay, e.g. Feline immunodeficiency virus (FIV) env and gag genes and birofilaria immitis p39 and 22kd are useful to detect feline immunodeficiency caused by FIV and to detect heartworm caused by D. immitis respectively.
                                                                                                                       Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
                                                                                                                                            pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PE binding/translocation domains-influenza A virus nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant swine pox virus - useful in vaccine for immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 37; DB 19; Length 499; 66.7%; Pred. No. 81; Live 2; Mismatches 1; Indels
                                                                   Swinepòx virus Hindill M fragment protein SEQ ID NO:231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 409-410; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR36821 standard; Protein; 917 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal against swine pox virus
                                                                                                                                                                                                                                                                                                                                                                   97WO-US12212.
                                                                                                                                                                                                                                                                                                                                                                                                                  8969890-S096
                       24-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cochran MD, Junker DE;
                                                                                                                                                                      Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYTR ) SYNTRO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-130677/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 enpahksq1 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV26105.
                                                                                                                                                                                                                       Swinepox virus.
                                                                                                                                                                                                                                                                   WO9804684-A1.
                                                                                                                                                                                                                                                                                                                                                                 25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-1996;
                                                                                                                                                                                                                                                                                                                     05-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR36821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR36821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
     0
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       digestive disease; Auješzky's disease virus; pseudorables virus; vaccine; such herpesvirus; such perpessirus; swince influenza virus; hog cholera virus; vector; porcine respiratory and reproductive syndrome virus; nucleoprotein; SIRSV; swine infertility and respiratory syndrome virus;
                                                                                                                                                                                                                                                                                                                                                                                                                  Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV; HCV:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from Anjeszky's disease virus, swine influence virus (SIV), portine respiratory and reproductive syndrome virus (PRBSV), hog cholera virus (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. This sequence represents the SIV strain H3N2 nucleoprotein. The coding sequence was subcloned into the plasmid pVRIO12 to generate plasmid pPB132 for use in the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \begin{tabular}{ll} Multi-valent polynucleotide vaccines against porcine pathogens - consist of at least 3 plasmids able to express protective antigens \\ \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a multivalent vaccine for protecting pigs
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 37; DB 19; Length 498; 66.7%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
     Indels
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAWJ5986 standard; Protein; 499 AA.
                                                                                                                                                                                                                       AAW68407 standard; Protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Fig 12; 63pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                                                      SIV strain H3N2 nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96FR-0009338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96FR-0009338
                                                                                                                                                                                                                                                                                                                  18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%
...as 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INMR ) RHONE MERIEUX SA.
     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from specified viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swine influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-112824/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 enpahksql 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498 AA;
                                                                                                320 enpahksql 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNPQHKTOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV49301.
                                                 1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FR2751224-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW55986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                      AAW68407;
```

Gaps

.; 0

RESULT 11

AAW55986

```
nucleoprotein; NP; PCR; amplification; translocation;
                                                                                                                                                                                   WPI; 1993-087107/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         734 enpahksql 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                             N-PSDB; AAQ38411
              binding; domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200044906-A2.
                                                                                                    09-SEP-1991;
                                                                               02-SEP-1992;
                                                                                                                                                 Donnelly JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000.
                                                          17-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                  EP532090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB15944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB15944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleoprocein gene (NP) cloned into the EcoRI site of pBR322.

A fragment containing the NP gene was obtained from the plasmid by PCR with primers that added a SacII site adjacent the Arg codon of NP, and the last 5 amino acids of PE followed by a termination codon and an EcoRI site to the 3' end of NP. The PCR fragment was digested with SacII and EcoRI and ligated to SacII/EcoRI-digested plasmid pVC-PEMI-2 (encoding a Pseudomonas exotoxin-influenza A virus MI matrix protein fusion). In the resulting plasmid, pVC-PENPcSaa, the binding and translocation domains of PE are fused
                                                                                                                                                                                                                                                                                                                                         Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful as vaccines against viral infections, tumours and
                                                                                        /note- "amino acids 2-414 of PE domains 1 and II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PE binding and translocation domains - Influenza A nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein; fusion; hybrid; pVC-PENPcSaa; pApr501; pBR322; pVC-PEM1-2;
Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus; NP; anti-viral agent; Pseudomonas exotoxin; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 37; DB 14; Length 917; 66.7%; Pred. No. 1.5e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                        Hawe LA, Liu MA, Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pApr501 was constructed from the influenza A virus
                                                                                                              /note- "influenza A virus Nucleoprotein"
                                                                                                                                     /note= "last 5 amino acids of PE"
                                                                                                                                                                                                                                                                                   Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Page 63-67; 81pp; English.
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR32469 standard; Protein; 917 AA.
                                                                                                                                                                                                                                                                                    Shi X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the Influenza A nucleoprotein.
                                  Chimeric Pseudomonas aeruginosa.
                                                                                                                                                                                                       92EP-0310067.
                                                                                                                                                                                                                             910S-0792507.
                                              Chimeric Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                         Friedman A,
                                                                                                                                                                                                                                                                                    Montgomery DL, Oliff AA,
                                                                                                                        .917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                   415..912
                                                                                                                                                                                                                                                  (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                        WPI; 1993-154266/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 enpahksgi 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ41728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein.
                                                                                                                                                                                                       04-NOV-1992;
                                                                                                                                                                                                                              08-NOV-1991;
                                                                                                                                                                                                                                                                         Donnelly JJ,
                                                                                                                                                                                12-MAY-1993
                                                                                                                                                           EP541335-A.
                                                                                                                                                                                                                                                                                                                                                                 parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR32469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                Region
                                                                                                    Region
                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR32469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
```

```
Example 25 describes the construction of pvC-PENPcSaa. A fragment contg. the nucleoprotein (NP) of Influenza A virus was obtained from plasmid pApr501. PApr501 is the nucleoprotein gene cloned into the EcoRI site of pR8222, by PCR with oligonucleotide primers which added a SacII site adjacent to the ATG codon of NP to give the sequence of AAQ38409, and the last 5 amino acids of PR followed by a termination codon and an EcoRI site to the 3' end of NP to give the sequence shown in AAQ38410. The PCR fragment was digested with SacII and EcoRI. The resulting plasmid pvC-PEMI-2 digested with SacII and EcoRI. The resulting plasmid is named pvC-PENPCSEAB. The S' and 3' ends of the PRNPSaa insert (AAQ38411) were verified by sequencing. This construction fuses the binding and translocation domains of PE to the Influenza A nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial toxin-antigen protein conjugates - to elicit cytotoxic T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. coli proliferation associated protein sequence SEQ ID NO:301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 14; Length 917; 66.7%; Pred. No. 1.5e+02; Ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                           , Liu MA, Marshall MS; Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 66-70; 85pp; English.
                                                                                                                                                                                                                                           Friedman A, Hawe LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB15944 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                 Shi x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2000; 2000WO-US02200.
92EP-0202660
                                                                            91US-0756249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                 Montgomery DL, Oliff Al,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                              (MERI ) MERCK & CO INC.
```

Gaps

```
Sednence
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                           ð
ö
                                                                                                                                                                                                                                                                                                        identify a proliferation- required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                                                                                                                            AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA66890 to AAA66055 and AAB16886 to AAB168040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA666055 and AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to
                                                   Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodman HM, Mahajan-Miklos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a virulence factor encoded by ORF14991.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virulence, factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pathogen; virulence polypeptide; virulence factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY29160 standard; Protein; 132 AA.
                                                                                                                                                                                     Claim 11; Page 224; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cao H, Drenkard E,
Tan M, Tsongalis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US25247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0066517.
99US-0117405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPT; 1999-357851/30.
                                                                  Xu HH;
                                                                                            WPI; 2000-514822/46.
                                                                                                                                                                                                                                                                                                                                                                                                       104 AA;
                                                                                                         N-PSDB; AAA65949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 pqhktel 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                з РОНКТОГ 9
27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1998;
                                                                Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ausubel F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahme LG,
                                                      Zyskind J,
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY29160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
AAY29160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
ö
                                                         The present sequence represents a Pseudomonas aeruginosa polypeptide sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                 note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.6%; Score 36; DB 20; Length 132; 62.5%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 6, 2002, 16:52:55 Job time: 337 sec
Disclosure; Fig 3; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not entirely correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 dnprhrsq 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DNPQHKTQ 8
```

```
US-09-232-468A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Appl
Sequence 24, Appl
                                                                                                                                                                        August 6, 2002, 16:53:56 ; Search time 51.22 Seconds (without alignments) 4.292 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 229,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application of the sequence 16, Personal Sequence 16, Personal Sequence 16, Personal Sequence 23, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 231,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cqn2_6/ptodata/2/iaa/GCOMB.pep:*
/cqn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-232-468A-18

US-09-232-468A-24

US-08-66-66-23

US-08-109-637A-229

US-08-102-863-11

US-08-102-863-11

US-08-758-621-14

US-09-107-858-14

US-08-758-621-14

US-08-052-681-4

US-08-052-681-4

US-08-052-681-4

US-08-474-067-5

US-08-474-068A-5

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-276-099A-16
US-08-781-890-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-405-647B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-985-499-16
PCT-US96-03180-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US93-03076-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-858-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-03076-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                  US-10-020-139-2_COPY_237_245
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                        1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                               Sedneuce:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
```

```
Sequence 2, Appli
Sequence 10, Appl
Sequence 6, Appli
Sequence 2, Appli
                                     Appli
Appli
                                                                         Appli
Appli
                                                                                                  Appli
Appli
Appli
                                                                                                                                     Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    US-09-232-468A-18
Sequence 18, Application US/09232468A
Patent No. 6207165
GENERAL INFORMATION:
APPLICANT: AUDONNET et al.
TITLE OF INVENTION: FOLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AUDONNET et al. TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
Sequence
Sequence
                                     Sequence
Sequence
                                                                         Sequence
Sequence
                                                                                                              Sequence Sequence 6
                          Sequence
                                                              Sequence
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 37; DB 4; Length 498; 66.7%; Pred. No. 27; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.5%; Score 37; DB 4; Length 498;
                                                            US-09-300-681B-2
US-09-284-033-2
US-09-729-834B-2
US-08-419-652-7
US-08-419-652-7
US-08-765-081-6
US-09-089-082-6
PCT-US95-06994-7
US-09-371-913A-7
                                                                                                                                                                          US-08-393-333-2
US-09-087-465-10
US-07-797-556-6
US-07-943-843-2
            US-08-729-834B-5
US-09-300-681B-5
US-09-300-681B-4
US-08-747-788-2
                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                    FILE CEFERENCE: 444313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DAFE: 1999-01-05
NUMBER OF SEO ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-232-468A-24

Sequence 24, Application US/09232468A

; Patent No. 6207165

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: swine influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: swine influenza virus US-09-232-468A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.5
Best Local Similarity 66.7
Matches 6; Conservative
  794
1001
1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 ENPAHKSOL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DNPOHKTOL 9
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.6%; Score 36; DB 4; Length 132; 62.5%; Pred. No. 10; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 37; DB 4; Length 498; 66.7%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahmejan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                      APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML NV0866,968C
CORRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PLENTIN Ver. 2.1
; SOFTWARE: PLENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
66.7%; Pred. No. 27; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/199,637A CURRENT APPLICATION NUMBER: US/09/199,637A CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,517 NUMBER OF SEQ ID NOS: 437 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 229, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                   Sequence 231, Application US/08686968C; Patent No. 6221361
GENERAL INFORMATION: APPLICANT: COCHEAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.65
Best Local Similarity 62.55
Matches 5; Conservative
  Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Swinepox virus
US-08-686-968C-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| ||:||
320 ENPAHKSQL 328
                                                                                   :11 [1:1]
320 ENPAHKSQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                             1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DNPQHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 DNI RHRSQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DNPQHKTQ 8
                                                                                                                                                                RESULT 3
US-08-686-968C-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-199-637A-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-199-637A-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                 à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.7%; Score 34; DB 1; Length 412; Best Local Similarity 62.5%; Pred. No. 77; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                               CONSTITUTIVE
EXPRESSION OF P450SOY
AND FERREDOXIN-SOY IN
STREPTOMYCES
                                                                                                                                                                                                                                        ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CUSTWARE: Version #1.25 CUSTRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/102.863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application PC/TUS9210885
GENERAL INFORMATION:
APPLICANT: SARIASLANI, SIMA
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  Sequence 11, Application US/U8102863
Patent No. 5466590
GENERAL INFORMATION:
                                                                                             APPLICANT: SARIASLANI, SIMATITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: AND FERRES TITLE OF INVENTION: STREPTOMY NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 302-552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                     WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                           DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 DDPEHNTQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DNPQHKTQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
PCT-US92-10885-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
RESULT 5
US-08-102-863-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-102-863-11
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
ORGANISM: Arabidopsis thaliana US-09-107-858-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Win
                                                         : 345 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14
                INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3
Matches 5; Conservative
(617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       King of Prussia
                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                , MOLECULE TYPE: protein US-08-758-621-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            |||:||
| 110 DNPRHK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 DNPRHK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DNPOHK 6
                                                                                                                                                                                                                                                                        1 DNPQHK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΡA
                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-858-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                Query Match
                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                             QD
                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Guerinot, Mary Lou, and Eide, David J. TTLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 34; DB 5; Length 412; 62.5%; Pred. No. 77; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                         OPERATING SYSTEM: Macintosh System, 6.0 SOFTWARE: Microsoft Word, 4.0 CURRENT APPLICATION DATA: APPLICATION NAMBER: PCT/US92/10885 FILING DATE: 19921216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Silveri, Jean M. REGISTRATION NUMBER: 39,030 REFERENCE-DOCKET NUMBER: DCI-099CP TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                   CR-9000-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/758,621
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08758621; Patent No. 5846821; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/POCKET NUMBER: CR-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 11:
        1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                        302-892-7342
302-892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
pCT-US92-10885-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                             COMPUTER: Macintosh
OPERATING SYSTEM: MA
                          WILMINGTON
DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 DDPEHNTQ 113
                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DNPQHKTQ 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                 19898
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-758-621-14
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

```
Gaps
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-0990FDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
EARLIER FILING DATE: 1998-06-30
BARLIER FILING DATE: 1208-06-30
BARLIER FILING DATE: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                     .
0
64.7%; Score 33; DB 2; Length 345; 83.3%; Pred. No. 97; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.7%; Score 33; DB 4; Length 345; 83.3%; Pred. No. 97; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodolas, Robert
APPLICANT: Stodolas, Robert
NITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-858-207A-318
Sequence 318, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09107858 Patent No. 6162900
```

```
APPLICANT: Kazunori YAMADA et al.
TITLE OF INVENTION: NOVEL PROTEIN HAVING NITRILE HYDRATASE
TITLE OF INVENTION: ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR PITLE OF INVENTION: FROM NITRILES VIA A TRANSFORMANT CONTAINING THE GENE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.7%; Score 32; DB 1; Length 115; 100.0%; Pred. No. 48; Uive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08052681
Patent No. 5314819
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           STRAIN: Rhizobium sp. MC12643
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20002
                                                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 DNPQH 81
                                                                                                                                                               HYPOTHE'LICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DNPQH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL, TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-052-681-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
                                                                                                                                                                                                  ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-052-681-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kazunori YAMADA et al.
TITLE OF INVENTION: NOVEL PROPEIN HAVING NITRILE HYDRATASE
TITLE OF INVENTION: ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR PROF
TITLE OF INVENTION: FROM NITRILES VIA A TRANSFORMANT CONTAINING THE GENE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.7%; Score 32; DB 4; Length 85; Best Local Similarity, 100.0%; Pred. No. 35; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                               UMBER: US/08/858,207A
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/052,681
                                                                     FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INVERMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                              P50475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08052681 Patent No. 5314819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/OR OFFICE TAILOR TO THE THE TAILOR TO THE TAILOR TO THE TAILOR TO THE TAILOR TO THE TAILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 318:
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: No. 6348328e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                             610-270-4478
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 DNPQH 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-858-207A-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DNPQH 5
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-052-681-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
```

Gaps

```
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-474-067-5
                             US-08-474-067-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 62.7%; Score 32; DB 1; Length 116; Best Local Similarity 100.0%; Pred. No. 48; Matches 5; Conservative 0; Mismatches 0; Indels
                OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,681
FILING DATE: 19930427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium sp. MC12643
                                                                                                                                                                                                    33,367
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4:
IBM Compatible
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       Warren M. Cheek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                  FILING DATE: 19930427
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL TYPE:
 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE:
PAGES:
```

78 DNPQH 82

1 DNPQH 5

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%; Score 32; DB 2; Length 712; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,067

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/213,361

FILING DATE: 14-MAY-1994

PRIOR APPLICATION NUMBER: US 07/607,293

FILING DATE: 30-OCT-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite 700
                                                                    APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE CAMPBell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1682
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08474067
Patent No. 5811518
Sequence 2, Application US/08474067; Patent No. 5811518
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 712 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.v
Est Local Similarity 6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-474-067-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United State 21P: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
                                                                                                                                                                                                        San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 OHKTOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QHKTQL 7
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.7%; Score 32; UB 2; Length 712; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                          PADPLICATION NUMBER: US 07/607,293
PILING DATE: 30-007-1990
ATTORNEYAGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1682
TELECOMMUNCATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-LJ 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/474,068A FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/213,361
FILING DATE: 14 MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                      APPLICATION NUMBER: US/08/474,067 FILING DATE: 07-JUN-1995
                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08474068A
; Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-L TELECOMMUNICATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 712 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0
ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-474-067-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Diego
                                                                                                                 FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 QHKTQL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111111
2 QHKTQL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-474-068A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

```
Gaps
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 712;
                                                                                                                                                                                                     Length 712;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
PC-DOSTAGENING SYSTEM: PC-DOSAMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%; Score 32; DB 2; Le 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                 Query Match 62.7%; Score 32; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6: Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,068A
CLASSIFICATION 514
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 14 MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P-LJ 1683
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/08474068A
; Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 712 amino acids
amino acid
                                                               : 712 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100. Matches 6; Conservative
                                                                                                                       , MOLECULE TYPE: protein US-08-474-068A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QHKTQL 9
                                                                                                                                                                                                                                                                                        , 4 QHKTQL 9
                                                                                                                                                                                                                                                                                                                             2 QHKTQL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 OHKTOL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-474-068A-5
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-474-068A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                   a
```

Search completed: August 6, 2002, 16:53:57 Job time: 289 sec

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

August 6, 2002, 16:52:58 ; Search time 32.88 Seconds (without alignments) 293.223 Million cell updates/sec

US-10-020-139-2 Title: Perfect score: Sequence:

1 MLQLWKLVLLCGVLTGTSES......NV1QQVVDNPQHKTQLQTLI 249

Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		P07743 mus musculu		рошоц	sacch	staphy	S	mycoplas			haemoph		tomato	tomato	sacchar					Е		Д		S	S	P42971 bacillus su		~		O		homo sanie	listeria	ccharom
SOFTHERNIES	ID		PSP_MOUSE	PLUN_MOUSE	LGN	YJK9_YEAST	ALF_STACA	ALM1_SCHPO	P200_MYCGE	TOXA_CLODI	EG5_HUMAN	DNLJ_HAEIN	RRPO_TOMK2				YGX7_YEAST	RA50_METJA	YQ38_CAEEL	RRP5_YEAST	NIFK_METMP	LBP_HUMAN	٠,١	NI80_YEAST	YKD3_YEAST	VGLF_SV5		RRPO_TOMK1				$LA0_{-}$	RYR2_HUMAN	ISPG_LISMO	YIM9_YEAST
	OB		7	-	П		-		Н	-	_	1	П	П	7	-	ч	Н	П	~	7	_	-	-	-	-4 -	٠,	٠,	۰,	-	н	-	-	_	_
	Length	-	235	~	25	9	53	$^{\prime\prime}$	61	71	0.5	67	61	_	61	ഹ	9	00	3	72	9	æ	9	98	m	N '	9	-10	4	υ.	3	33	S	36	<u></u>
oN	Query Match		29.6	S	4	æ. œ.	9.8	ω .υ	8.4	8.4	8.1	8.0	၀. အ	0.0	0.8	7.9	7.9	7.8	7.7	7.7	7.6	7.6	9.7	7.6	7.6	۷. ۱	٠. د .	ر ر د ر	ر. ن	. i	7.5	7.4	7.4	7.4	7.4
	Score		364.5	9	8	109	_	104.5	104	104	100		യ	98.5	മാ	67	6	96		94.5	94	94		93.5	າ ເ	V (N (V	200	76		91.5	_	91	91
	Result No.		 1	7	m ·	4	2	9	7	ω	σ,	10	11	12	13	14	15	16	17	18	9.	20	21	22	57	7 (0.0	9 10	770	87	67	30	31	32	33

P16573 rattus norv	O67606 aquifex aeo	049460 mycoplasma	009793 schizosacch	O58556 methanococc	09v7a4 drosophila	P12612 saccharonyc	010339 schizosacch	063313 rattus norv	Ogusi6 schizosacch	P46939 homo sapien	P49022 lactococcus
ECTO_RAT	METE AOUAE	Y468_MYCGE	NG79_SCHPO	YB56_METJA	ITA4 DROME	TCPA_YEAST	YBM2_SCHPO	LBP_RAT	MYS2_SCHPO	UTRO_HUMAN	PIP_LACLA
7	-	~	7	_	7	_	-	-	_	_	
519	761	1783	425	903	1015	559	615	481	1526	3433	901
7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2
2	٠. د	0.5	90	90	90	89.5	89.5	68	68	8	88.5
90.	6	Q,									

ALIGNMENTS

PEDULT 1 PSP_MOUSE STANDA AC P07743; DT 01-AUG-1988 (Rel. 08, 01-AUG-1988) RM SEQUENCE FROM N.A. RC TISSUE-PATCHIG Gland; RX MAGSEN H.O., Hjorth J. RC TISSUE-PATCHIG Gland; RX MAGSEN H.O., Hjorth J. RY "MOIECULAR CLONING OF RY "MOIECULAR COORDING OF MUTH THAT OF SALIC CC "THE SWISS IN "COORDING TO FORTH THAT OF SALIC CC "THE EUROPEAN BIOLING TO FORTH THAT OF SALIC CC "THE EUROPEAN BIOLING TO FORTH SALIC CC "THE EUROPEAN BIOLING TO FORTH SALIC CC "THE EUROPEAN BIOLING TO FORTH SALIC CC "THE EUROPEAN BIOLING TO SENDE, MOIES PROPER EMBL: M26807; CAA2584 (MOIES MOIES PROPE) REMBL: M26807; CAA2584 (MOIES MOIES MOIES MOIES MOIES SIGNAR MOIES MOIES MOIES SIGNAR MOIES MOIES SIGNAR MACCHER SIGNAR SIG	DOUSE PSPE_MOUSE STANDARD; PO743; DO1-AUG-1988 (Rel. 08, Last D1-NOV-1997 (Rel. 35, Last PSPE. D1-NOV-1997 (Rel. 35, Last PSPE. MAGGO 1988 (Rel. 08, Last PSPE. MAGGO 1988 (Rel. 08, Last PSPE. MAGGO 1988 (Rel. 36, Last PSPE. MAGGO 1987 (Rel. 35, Last PSPE. MAGGO 1987 (Rel. 35, Last PSECUENCE FROM N.A. TISSUE-Parotid gland; MAGDINE-85215456; Pubmed-25 MAGBOLINE-85215456; Pubmed-25 MAGBOLINE-85215456; Pubmed-25 MAGBOLINE-8704556; Pubmed-25 MAGBOLINE-870456; Pubmed-25 MAGGO 17, Hjorth J.P.; NOCORTION: PSP IS THE MOST NO TIS FUNCTION IS NOT KNO MITH THAT OF SALIVARY A MITH THAT OF SA	PRT; sequence u annotation orecursor (ta; Craniat ia; Sciurog be PSP mRNA. (1985). (1986). (ppdate) update) update) update) update) sa; Vertebrat finathi; Muric formatics a k K., and salivary and salivary THE PAROTID GLANI CTION IS COORDINAN d through a collak not the EMBL outst not restrictions content is in or restrictions content is in for con for www.isb-sib.ch/ar NFC64; Length 235; Indels 17; Gap	
ARD; PRT: 235 AA. "Created) "Last sequence update) "Last annotation update) "Chordata: Craniata: Vertebrata: E Rodentia: Sciurognathi: Muridae; "M.M.A. "M.M.A. "D.P.; "A mikkelsen B.M., Harmark K. "J.P.; "B.K., Mikkelsen B.M., Harmark K. "J.P.; "M.M.A. "D.P.; "M. M.A.	PRT; 235 AA. sequence update) annotation update) arcursor (PSP). 22 Craniata; Vertebrata; Euteleo a; Sciurognathi; Muridae; Murina (PSP mRNA."; 1985). 28613; Mikkelsen B.M., Harmark K., Otid secretory protein and salive otid secretory protein and salive stransport of the propertion of the properties of the propertion of the properties of the proper	pdate) update) update) s; Vertebrata; Euteleo mathi; Muridae; Murina Lory protein and salive tory protein and the EMM: There are no restriction as its content in and as its content in and the EMM: There are no restriction (See http://www.isb-si h): L. SECRETORY PROTEIN. ARIBGEZEF3 CRC64; A+5; DB 1; Length 235 tohes 80; Indels 1	k K., and salive THE PAROTI CTION IS CC through and the EM no trestri content is e by and /www.isb-si content is content	

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ICR, TISSUE-Palate;
MEDLINE-9240770; PubMed-10224143;
Weston W.M., LeClair E.B., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma.L., Tunk R.S., Greene R.M.;
"Differential display identification of plunc, a novel gene expressed in embryonic palate, nasal epithalium, and adult lung.";
Bool. Chem. 274:13698-13703(1999).
                                                                                                                                                                                                                                                                             166 DKISJSULGRKUP1INSILDGVSTULTSTVLQNPICPLLQYVUSTUNPSVLQGLISN 225
                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN"TDIFG--LKISNSLILDVKAEPID 118
                                                                                                                      49 DVELLQQATSWPLAKNSILET --- LNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSS 105
                                                                                                                                                                   119 DGKGLNLSFPVTANVTVAGPIJGQIJNLKASLDLLTAVTJETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                         106 NGNGIDLTVPLAGEASLYLPFICKTVDISVSLDLINSLSIKTNAQTGLPEVTIGKCSSNT 165
                                                                                                                                                                                                                                                      179 TSISESELDKHSOIINKFVNSVINTEKSTVSSELQKEICPEIRFFIHSEDVNVIQQVVDN 238
                        1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic organization of the mouse plunc gene and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             after exposure to irritants. May be associated with tumor progression (By similarity).

-- SUBCELLULAR LOCATION: Secreted (By similarity).

-- TISSUE SPECIFICITY: Upper airways, nasopharyngeal regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: May be involved in the airway inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeClair E.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weston W.M., LeClair E.E., Trzyna W., McHigh K.M., Nugent P. Lafferty C.M., Ma L., Tuan R.S., Greene K.M.;
J. Biol. Chem. 275:8262-88262(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 284:792-797(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21290678; PubMed=11396972;
                                                                                                                                                                                                                                                                                                                                                                                                                                            6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF356785; AAK63069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developing airways and thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U69172; AAB63256.1; -. MGD; MGI:1338036; Plunc.
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pepeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thymus.
                                                                                                                                                                                                                                                                                                                                                                                                      PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                  PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                               ŏ
                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                    ò
                                                                                  òγ
```

```
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLLDKHSGIINK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 PVVGSLLQLAVKLNITAEVLAVKDNQGRIH---LVLGDCTHSPGSLKISLLNGVTP-VQS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SPALPSNPTDLLAGKFTDALSGGL-----LSGGL-----LG1LENIPLLDVIKSGGN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AEKLLNNVISKL---LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein Plunc precursor (Palate lung and nasal epithelium clone protein) (Lung specific X protein) (Nasopharyngeal carcinoma-related protein) (Tracheal epithelium enriched protein).
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                            1 MFLVGSLVVLCGLLAHSTAQLAGLPLPLGQGPPLPLNQGPPLPLNUGQLLPLAGGLPLAV 60
                                                                                                                                                                                                                                                                                                                                                                                                  30 ----SNVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iwao K., Watanabe T., Fujiwara Y., Takami K., Kodama K., Higashiyama M., Yokouchi H., Ozaki K., Monden M., Tanigami A.; Insolation of a novel human lung specific gene, LUNX, a potential molecular marker for detection of micrometastasis in non-small-cell
                                    4 X 6 AA KEPEATS OF G-[1,PQ]-[PL, -1,-P-1,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of the human plunc gene, a gene product with an upper airways and nasopharyngeal restricted expression pattern,"; Biochim. Biophys. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     N-LINKED (GLCNAG. . .) (POFENTIAL)
N-LINKED (GLCNAG. . .) (POFENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         He Z.W., Yao K.T., Xu L.G., Ren C.P., Lan K., Xie L., 2hang L.,
Liu W.D., Zhou W., Wang L.;
                                                                                                                                                                                                                                                                               91:
                                                                                                                                                                                                                                         DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 FVDNLTGILTKYLPELIQGKVCPLVNGILSGLDVTLVHNIAELLIHGLQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                             49; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                      ---NLGNDL----
                                                                                                                                                                              7F40BED9859188FB CRC64;
                                                                                                                                                                                                                                     15.8%; Score 194.5; DB 1
23.5%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09NP55; 09NZT0;
16-0CT-2001 (Rel. 40, Created)
10-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA
                   PROTEIN PLUNC
POTENTIAL
                                                                                                                                                                                                                                                                                                                      1 MLQLWKLVLLCGVLTGTSESLLD-------
                                                                              REPEAT 2
                                                                                                                    REPEAT 4
                                                           REPEAT
                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20472055; PubMed-11018263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21150203; PubMed-11251963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Cancer 91:433-437(2001).
                                                                                                                                                                              28611 MW;
                                                                                                                                                                                                                                                          Best Local Similarity 23.59
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bingle C.D., Bingle L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_Tax LD=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLUNC OR LUNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLUN_HUMAN
                                                                                                                                                                                                                                         Query Match
                                                                                                                                       CARBOHYD
                                                                                                                                                             CARBOHYD
                                                                                                                                                                                SEQUENCE
                   CHAIN
DOMAIN
                                                                          REPEAT
REPEAT
                                                           REPEAT
                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

. 9

```
RA SEQUENCE FROM N.A.

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagquley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beare D.M.,
Baley D., Burrill W., Buller Bakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Carter N.P.,
Carder N.P.,
Cooley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson C.M., Johnson C.M., Johnson C.M., Johnson C.M., Johnson C.M., Martin S.L., McConnachie L.J., McLay K., Martin S.L., McConnachie L.J., McLay K., McMarty A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Philimore B.J.C.T., Prathalingam S.R., Park, Ramsay H.,
RA Rich C.M., Ramsay R.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tronans A.C., Vaudin M., Wall M., Wallis J.M., Thorpe A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung nasal epithelial clone protein, in human nasal lavage fluid with two-dimensional electrophoresis and matrix-assisted laser electrophoresis 22:1795-1800(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Upper airways and nasopharyngeal regions, including trachea and nasal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21317946; PubMed=11425234;
Lindahl M., Stahlbom B., Tagesson C.;
"Identification of a new potential airway irritation marker,
"Civoling a new gene related to nasopharyngeal carcinoma.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN PLUNC.
Q -> K (IN REF. 1; AAF70860).
EDF152FBC35315BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 95-152; 157-167 AND 214-232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and some other types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF214562; AAG13653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF172993, AAF70860.1)-
EMBL, AB024937, BAA93633.1)-
EMBL, AF188745, AAF92622.1,
EMBL, AL121901, CAC03549.1,
EMBL, BC012549, AAH12549.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE~Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 2:
220 2:
256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial ortities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                   75 KOKAQEAEKLLNNVISK----LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                  46; Mismatches 100; Indels 33; Gaps
                                                                                                                                                                  78 KPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSPDGHKLVVTIPLGI 137
                                                                                                                                                                                                132 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                              138 KLQVNTPLVGASLLRLAVKLDITAEILAVRDKOERIHL-VLGDCTHSPGSLQISLLDGLG 196
                                                                       15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                                     45 TGLAGSLTNALSNGL-----LSGGL------LGILENLPLLDIL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 37.5 kb region of yeast chromosome X includes the SMEI, MEF2, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar Yeast 11:873-883(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 SILTFLDKEDKPVCDKFITSYTRSIARYDRS-----KLNIILSLLKK-----IRLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 79
                                                                                                                                                                                                                                                             191 QI-INKEVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                     197 PLPIQCLLDSLTGILNKVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
                  14.9%; Score 183.5; DB 1; Length 256; 23.8%; Pred. No. 7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 200.0 kDa protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 109; DB 1; Length 1769; 19.2%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 064480D1D249B241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / FY1679;
MEDLINE=96090136; PubMed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000357; HEAT_repeat
PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200080 MW;
Ouery Match
Best Local Similarity 23.8%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X85021; CAA59385.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA89404.1; -.
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S0003645, YJL109C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1769 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasmussen S.W.;
                                                                                                                                                                                                                                                                                                                                                                          YJK9_YEAST
P42945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                        YJK9_YEAST
                                                                                                                                     ò
                                                                                                                                                                   q
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                          191 QIIN-----KFVNSVINTLKSTVSSLLQKEICP 218
                                                                                                                                                                          474 ELINTINVSMLJETGERYKKVLSLFTEAIGKGYKASSFLTSFFTTLESRITFLLRVTISP 533
80 EAEKLLNNV1--SKLLPTNTD1----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 132
                                379 EVRLIITDLIYLSEILEDKSQLVELFEYFISINEDLVLKCL-----KSLGLT----- 425
                                                                     133 VIVAGPIJGQIINLKASLDLLTAVTIETD - PQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                     426 -----GELFEIRLTTSLFTNADVNTDIVKQLSDPV----ETTKKDTASFQTFLDKHS 473
                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. BACTORIOL. 175:7485-7489(1993).

-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate - glycerone phosphate - b-glyceraldehyde 3-phosphate.
-!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
-!- PATHWAY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHIFF-BASE WITH DIHYDROXYACETONE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
A189E75574FIFCCO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus carnosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noscription in the property of the property of property of proporty, divolving centry; 1. Probom; PD001128; Aldolase_II. Proporty; PS001158; Aldolase_II.; FALSE_NEG. PROSITE; PS00158; ALDOLASE_CLASS_II; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       219 LIRIFIHSLDVNVIQOVVDNPQHKTQLQTL1 249
                                                                                                                                                                                                                                                       534 AAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol, 175:7495-7499(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=TM300;
MEDLINE=94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyage; Schiff base; Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 AA; 32720 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kula M.R., Brockamp H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S33358; S33358.
PIR; A49943; A49943.
HSSP; P14223; 1A5C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Witke C., Goetz F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Witke C., Goetz F.;
J. Bacteriol. 175:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carnosus."
                                                                                                                                                                                                                                                                                                                                                     ALF_STACA
007159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIE MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                    ALF_STACA
                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                            ŏ
                                                                                                                   g
                                                                                                                                                         ò
                                                                                  ò
```

```
the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation
                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20123449: PubMed=10660053; Jimenez M., Petit T., Gancedo C., Goday C.; Jimenez M., Petit T., Gancedo C., Goday C.; The alm1+ gene from Schlzosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
                                                                              52 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKILNNVISKILPTNTDIFGLKISNSLILD 111
                                                                                                                                                                                                                                              152 -----LLTAVTIET-----DPQTHQPVAVLGECASDPTSISLSLILDKHSQIINKF 196
                                                                                                                                                                                                                                                                                   203 KKDOYVMIKITIPTKVNAYSELJEHPQVIRVVALSGGYSRDEAN---KILKQNEGLIASF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.; submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             145 NNKEAIE--KVVKQQFEVAKEIIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 202
                                                                                                                        93 KGIVPFLKVDKGLAEEADGVQLMK-PIPDLDKLLDRA-----NEKGIFGTKM-KSNILL 144
                                           64; Indels 48: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,
CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of GFP-gene fusion library of fission
Ouery Match

8.6%; Score 106; DB 1; Length 295;
Best Local Similarity 25.9%; Pred. No. 0.5;
Matches 50; Conservative 31; Mismatches 64; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               090775; 013313; 090778;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ALMI OR SPACI486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL133357; CAB62414.1; *.
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; *.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               260 SRALVSDLNAQQS 272
                                                                                                                                                                                                                                                                                                                                        197 VNSVINTLKSTVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-968 H90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOKINESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ding D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                   qq
                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                           ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                               333 SENSIRELQEKYDSVVSELQVVKENKNTSVSAGVGLFSPLAQKLSAVQNPEFSFTKVYSD 392
                                                                                                                                                                                                                                                                             50 --TLKGILEKLKVDI,GVLQK--SSAWQLAKQ-----KAQEAEKLLNNVISKLLFTNTDIF 100
                                                                                                                                                                                                                                                                                                      393 NMKLQOKVSSLKLOLDKLTNKFSSFCEQVKORIPVVKOORSEIVRNNIYMNFLSES---- 448
                                                                                                                                                                                                                                                                                                                                    101 GLKISNSLILDVKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 159
                                                                                                                                                                                                                                                                                                                                                                449 - LETSNNNLTKVQAELLSTKMKQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSR 507
                                                                                                                                                                                                                                                                                                                                                                                            160 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 219
                                                                                                                                                                                                                                                                                                                                                                                                                    508 NVPATVQ--VALDEYAQNPSTASETLVNK--ELAN-----FSSIKEAVSKYLE----- 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton K.A., Flaser C.M., Gocayne J.D., White O., Adams M.D., Clayton K.A., Fleischmann R.D., Bult. C.J., Kerlavage A.R., Sutton G., Kolley J.M., Nuyen D.T., Weldman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Tomb J.-F., Dougherty B.A., Bott K.F., Phillips C.A., Merrick J.M., Peterson S.N., Smith H.O., Hutchison C.A. Intider T.S., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                   18 SESLLDNLGNDLSNVVDKLEPV------49
                                                                                                                                                                                                           61;
                                                                                                                                                                          DB 1; Length 1727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                             COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
COLLED COIL (POTENTIAL)
MW: F820BF8D9C132644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                   94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bedreits. 175:7918-7930(1993).
-!- FUNCTION: COULD BE A ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE (BY SIMILARITY).
                  COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1616 AA.
049429; 049259; 049298; 049352; 049353;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                 8.5%; Score 104.5; D
24.3%; Pred. No. 6.4;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
                                                                                                                       197858
                                                                                                                                                                                 24.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 IRIFIHSL--DVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 LREKVRALECDVEIGKOTV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                       Best Local Similarity 24.39
Matches 63; Conservative
                                             740
1106
1427
1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma genitalium.
                                                                                                                  1727 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2097;
 Colled coil.
                                                                                                                   SEQUENCE
                                                                                                                                                              Query Match
                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing.
                                           DOMAIN
                                                                                    DOMAIN
                                                           DOMAIN
                                                                        DOMAIN
                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P200_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
KW
FT
FT
FT
FT
FT
SQ
                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        461 SKEIKDSAKADLSNISDDIDSVWKEFGSFTDETQKSVEEKSQVDEIILDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQOEFSEPVVSDEKIKETNSDESVNTDL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 -~IFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQI--IN---- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 TALESEKLVNEVLL -- TNEYUD----VNAPFSTETEVKVSSELPKSELVDEITFINNDPK 631
                                                                                                                                                                                                                                                                                                                                                                                18 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 ----LKASLDLL-----TAVTIETDPQTHQPVAVL------GECASDPTSI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 POEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDISLELUSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLJRIFIHSLDVNVIQQVVDNPQH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 ELN----HEELGNEFIN-----716
                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- KLLPTNTD----- 98
                                                                                                                                                                                                                                                                                                                                                                  75; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                          Structural protein; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                 8.4%; Score 104; DB 1; Length 1616;
20.6%; Pred. No. 6.4;
tive 48; Mismatches 75; Indels 12
                                                                                                                                                                                                                                                                                     > F (IN REF, 2)
6AF76A13AC49E4FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-VPI 10463;
MEDLINE-90221894; PubMed-2109310;
Sauerborn M., von Elchel-Streiber C.;
Nucleotide sequence of Clostridium difficile toxin A.";
                                                                                                                                                                                                                                                                       P -> S (IN REF. 2).
S -> F (IN REF. 2).
                                                                                                                                                                                                                        1-2.
2 X 26 AA REPEAT.
                                                                                                                                                                                             2 X 32 AA REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                   EMBL, U02245, AAA03401.1; ALT_FRAME.
EMBL, U02175, AAD12458.1; -..
EMBL, U02126, AAD12402.1; -..
                                                                                                                                                                                                                                                                                                185678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     78 AQEAEKLLNNVIS------
                                                                                        EMBL; U39720; AAC71613.1; -.
                                                                                                          EMBL; U02245; AAA03400.1;
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium difficile,
                                                                                                                                                                                                                                                                                            1616 AA;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                         1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           1161
1310
256
304
                                                                                                                                                                                                                               891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 KTQLQT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      717 TTQLET 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1496;
                                                                                                                                                                       Cytadherence;
                                                                                                                                                            MG386;
                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOXA OR TCDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOXA_CLODI
P16154;
                                                                                                                                                                                                                                                                            CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                            TIGE;
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOXA_CLODI
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

us-10-020-139-2.rsp

```
receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NP_BIND
MOD_RES
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          867 VSDELYELKKLINNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKELFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            927 ITKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFJQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ11NKFVNSVINTLKSTVSSLLQKEI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807 KTLLLDASVSPDTKFILNNLKLNIESSIGDYIYYEKLEPVKNIIHNSIDDLIDEFNLLEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 57
                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833 AA REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF FIVE
                                                                                                                                                                                                                                                                                                                                                                                                                  -1- DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN ENTERCYTOXIN B. ONLY AFTER THE ENTERAL DELIVERY OF THE ENTERCYTOXIN A. MAY THE CHARACTERISTIC DISEASE CALLED PSEUDOMEMBRANOUS COLITIS BE INDUCED.
                                                                                                                                                           'Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 104; DB 1; Length 2710; 20.3%; Pred. No. 12;
                                                                                                          Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.3%; Pred. No. 12,
Conservative 63; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EG5.HUMAN STANDARD: PRT; 1057 AA. P5232: 015716; 01-00T-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 249
  Nucleic Acids Res. 18:1629-1630(1990).
                                                                          STRAIN=VPI 10463;
MEDLINE=90129305; PubMed*2105276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S08638; S08638; CM_binding.
InterPror; IPR002479; CM_binding.
Pfam; PF01473; CM_binding_1; 31.
Toxin; Enterotoxin.
                                                                                                                                                                                                          infect. Immun. 58:480-488(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X51797; CAA36094.1; -. EMBL; M30307; AAA23283.1; -. EMBL; X92982; CAA63564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            DIFFERENT OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                    STRAIN=VPI 10463;
von Eichel-Streiber C.;
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
EG5_HUMAN
                                                                                                                                                                                              dene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
         SOURTH TANKER TO THE THE TO THE THE TO THE T
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
Kinesin-related motor protein Eg5 (Kinesin-like spindle protein HKSP)
(Thyroid receptor interacting protein 5) (TKHP5) (Kinesin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L. Endocrinol. 9:243-254(1995).
FUNCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIFOLAR
SINDLE. BLOCKING OF EGS PREVENTS CENTROSOME MIGRATION AND ARREST
CELLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS.
SUBBUNIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE
                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A., PHOSPHORYLATION SITE THR-927, AND MUTAUFENESIS. MEDLINE=96128120; PubMed=8548803; Hlangy A., Lane H.A., D'Herin P., Harper M., Kress M., Nigu E.A.; Phosphorylation by p34cdc regulates spindle association of human Egs, a kinesin-related motor essential for bipolar spindle formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95295737; PubMed-7776974; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; "Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRESENCE OF THYROID HORMONE.

PTH: PHOSPHORYTCHATED EXCLOSIVELY ON SERINE DURING S PHASE, BUT ON BOTH SERINE AND THE-927 DURING MITOSIS, SO CONTROLLING THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
PHOSPHORYLATION (BY CDC2).
T->A: NO MITOTIC PHOSPHORYLATION NO
BINDING TO SPINDLE APPARATUS.
                                                                                                                                                                                     Eŭkaryola, Metazoa, Chordata, Craniata, Vertebrata, Euteleuskumi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whitehead C.M., Rattner J.B.; Expanding the role of the second post-mitolic "Expanding the role of Heggs within the mitotic and post-mitolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled coil; Mitosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E322F2141BEF1601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNS -> EL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98369052; PubMed-9701554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Sci. 111:255i-2561(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 1PRO01752; kinesin.
Pfam; PF00225; kinesin; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 819-868 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X85137, CAA59449.1; -. EMBL, U37426, AAA86132.1; -. EMBL, I.40372, AAC41739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 83:1159-1169(1995).
                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 67
1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLY PROPHASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P33176; 1BG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phases of the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364
737
105
927
927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT:
                                                                                                                      KNSL1 OR EGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 148760;
```

```
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER LINKAGES BETWEEN 5'-PHOSPHORYL AND 3'-HYDROXYL GROUPS IN DOUBLE-STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF DAMAGED DNA (BY SIMILARITY)

CATALYTIC ACTIVITY: NAD(+) + (deoxyribonucleotide)(N) + (deoxyribonucleotide)(M) = AMP + nicotinamide nucleotide)(A+M).
                                                                                                                                                                                                                                                                                        550 KDGSSKQKAMLEVHKTLFGNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                                                                                                                        182 SLSLLDKHSQ11NKF------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 228
                                                                                                                    447 LDQCKSDLQNKTQELE-----TTQKHLQETKLQL-VKEEYITSALESTEEKLH 493
                                                                                                                                                 80 E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 127
                                                                                                                                                                              494 DAASKLLNTVEE----TTKDVSGLHSKLDRKKAVDOHNAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=RD, KW20 / KW20 / Arcc 51907;
MEDLINE=95350630. PubMed=7542800;
MEDLINE=95350630. PubMed=7542800;
MELSCHMARD R.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Sauddek D.M., Brandon K.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                          70; Gaps
                                                                                       22 LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKI,KVDLGVLQK--SSAWQLAKQKAQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
                                                                                                                                                                                                            128 ----PVTANVTVAGPIIGQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA LICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                         8.1%; Score 100; DB 1; Length 1057; Similarity 24.4%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.^{\mathrm{H}};
                                                        79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        679 AA
                                                          34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGN OR LIG OR HIll00.
Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                   Local Sim.
59;
                                                                                                                                                                                                                                                                                                                                    229 VN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus
                                                                                                                                                                                                                                                                                                                                                                 650 IN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNLJ_HAEIN
P43813;
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             DNLJ_HAEIN
                                                           Matches
                                                                                                                                                     ò
                                                                                                                                                                             g
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                    9
```

```
RRPO_TOMK2 STANDARD; PRT; 1616 AA.
P89456. P90349.
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Methyltransferase/RNA helicase (EC 2.7.7.48) (183 kDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)].
Tomato mosalc virus (strain Kazakh K2) (TOMY) (TMY strain K2).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 KLLNNV------ISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 ANVIVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 VVIRRAGDVIPQII------GVLHERRPDNAKPIIF-----PTNCPVC---DS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 SLGYDIDGTVLKINDI-------ALQNELGFISKAPRWAIAYKFPAQEEL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51. Biol. (Mosk) 31:826-830(1997).
- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL.
- PRINCEPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA-KQKAQEAE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 TLLNDVEFQVGRTGAITPVAKLEP--VFVAGVTVSNATLHNG-----DEIERLNIAIGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 QIINKEVNSVINTLKSTVSSLLQKEICPLIRIFI--HSLDVN-----VIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K.; "Properties and structure of the tobacco mosaic virus strain K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 QIIRIEGEAVARCTGGLFCAAQRKE---ALKHFVSRKAMDIDGVGGKLIEQLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligase; DNA repair; DNA replication; NAD; Complete proteome. DOMAIN 601 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 99; DB 1; Length 679;
23.1%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.1%; Preq. nc.
Watches 54; Conservative 41; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                    InterPro; IPR001679; DNA_ligase_N.
InterPro; IPR004150; DNA_ligase_OB.
InterPro; IPR004149; DNA_ligase_ZBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50172; BRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
PROSITE; PS01056; DNA_LIGASE_N2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD003944; DNA_ligase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE~98012318; PubMed=9454068;
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00533; BRCT; 1.
Pfam; PF01653; DNA_ligase_N; 1.
Pfam; PF03120; DNA_ligase_OB; 1.
Pfam; PF031120; DNA_ligase_ZBD; 1.
Pfam; PF00633; HHH; HHH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 AA; 75188 MW;
                                                                  EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                                                                                                                                   interPro; IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00532; LIGANC; 1.
                                                                                                                                                                                                                                                                                     InterPro; IPR000445; HHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00292; BRCT; 1.
SMART; SM00278; HhH1; 2.
                                                                                                                                                         InterPro; IPR001357;
                                                                                                    1B04.
                                                                                             087703;
                                                                                                                                  H11100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POMK 2
```

```
EMBL; X02144; CAA26085.1; -.
                                                                                                                                                                                                                                                            EMBL; X02144; CAA26082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 20.49
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1616
1116
                                                                                                                                                                                                                                                                                     PIR; A04195; WMTM8T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
  SO THE TENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPO_TUME

AC PO3587: 041352;

DT 21-3UL-1986 (Rel 01, Created)

DT 21-3UL-1986 (Rel 01, dast enquence update)

DT 16-OCT-2001 (Rel 40, Last endotation update)

DT 16-OCT-2001 (Rel 40, Last endotation update)

DF RNA-directed RNA polymerase (EC 27.7.48) (183 kDa protein) [Contains: DE RNA-directed NNA helicase (MT/HEL) (126 kDa protein)].

DE Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)].

OS Tomato mosaic virus (strain L) (Towy) (Twy strain tomato).

Viruses: ssRNA positive-strand viruses, no DNA stage: Tobamovirus.
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA-----LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 1DDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPPING AND AN RNA HELICASE.
MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
-!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and comparison with the common strain genome."; J. Biochem. 96:1915-1923(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohno T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2F5CE0C8C965336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 98.5; 20.4%; Pred. No. 16
                                                                                                                                                                                                                                                                                                                              InterPro: 1PR001788; RNA_dep_RNApol2.
InterPro: 1PR001788; V_methyltransf.
InterPro: 1PR00568; V_methyltransf.
Pfam; PF00978; RNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833 840 ATE
1616 AA; 183614 MW;
                                                                                                                                                                                                                                                                                  EMBL; 292909; CAB07439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 YTGPLKVQQMKNF1DS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                              EMB1,: 292909; CAB07438.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ogykb6. Ogwu37;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last enrotation update)
16-0CT-2001 (Rel. 40, Last enrotation update)
16-0CT-2001 (Rel. 40, Last sequence (EC 2.7.7.48) (183 kDa protein) (Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)).
16-0CT-2001 (Rel. 40, Last enrotation (Toutains: Methyltransferase/RNA helicase (MT/HEL) (183 kDa protein)).
16-0CT-2001 (Rel. 40, Last enrotation)
16-0CT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSL1LDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVUP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLOKEICPLIRI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHMATASSLIHKQMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Zhou X., Xue C., Chen Q., Qi Y., Li D.; Zhou X., Xue C., Chen Q., Qi Y., Li D.; "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPPING AND AN RNA HELICASE.
MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; PF01660; Vmethyltransf: 1.
Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616
RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 98.5; DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).

IN; ASEC8929B5CF7CAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKT; 1616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.4%; Pred. No. 16;
tive 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00978; RNA_dep_RNAPo12; 1.
Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833 840 ATP
1616 AA; 183564 MW;
```

```
PRINTS; PR00195; DYNAMIN. SMART; SM00053; DYNC; 1. SMART; SM00302; GED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02212; GED; ]
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
244
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGX7_YEAST
P53076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGX7_YEAST
        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITE-994(05918; PubMed=8810043; Miosga T., Zimmermann F.K.; PubMed=8810043; Miosga T., Zimmermann F.K.; Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 Ab tragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CPTR."; Yeast 12:693-708(1996).
                                                                                                                                                                                                                                                                                                                                 57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                 640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHMATASSLIHKOMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                      117 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                         165 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 222
                                                                                                                                                                                                                                                                                                        44; Mismatches 79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammie A.E., Kurihara L.J., Vallee R.B., Rose M.D.;
"DNM1, a dynamin-related gene, participates in endosomal trafficking
                                                                                                                                      InterPros; IrROGUESO.
Pfam: PF00978; RNA_dep_RNApol2; 1.
Pfam: PF01443; Viral_Helicasel: 1.
Pfam: PF01660; Vmethyltransf: 1.
Transferase: RNA-directed RNA polymerase: Helicase: ATP-binding.
CHAIN 1 1616 METHYLTRANSERSE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                               DB 1; Length 1616;
                                                                                                                                                                                                                            40 ATP (POTENTIAL).
183542 MW; 5DBBFB2FADCC5COC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
DNM1 OR YLL001W OR 1.1381.
                                                                                                                                                                                                                                                                               Match 8.0%; Score 98.5; I Local Similarity 20.4%; Pred. No. 16;
                                                                                                       InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C;
MEDLINE=95348179; PubMed=7622557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in yeast.";
J. Cell Biol. 130:553-566(1995).
                                                                                EMBL; AJ132845; CAB36997.1; -. EMBL; AJ132845; CAB36998.1; -.
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 FIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                             840
                                                                                                                                                                                                                            833 84
1616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288C / FY23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNM1_YEAST
P54861;
                                                                                                                                                                                                                            NP_BIND
SEOUENCE
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
DNM1_YEAST
                                                                                                                                                                                                                                                                                                         Matches
     ó
                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation her European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 QLAKQKAQEAEKLLNNVISKLLPTNTDIF------GLKISNSLILDVKAEPID 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 -----OTEQELARYGGVGATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 SESLKLAREVDPQGKRTIGVITKLD-LMDSGTNALD-ILSGKMYPLKLGFVGVVNRS--- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 SESL-----LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD-LGVLQKSSAW 71
Vandenbol M., Portetelle D., Hilger F.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MICROTUBLE-ASSOCIATED FORCE-PRODUCING PROTEIN THAT PARTICIPATES IN ENDOCYTOSIS. DOES NOT.APPEAR TO PARTICIPATE IN SECRETION OF VACUOLAR PROTEIN SORTING.
-!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
-!- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 ---QQDJQ-----ENKTVEESLDKEEDYFRKHPVYRTISTKCGTRYLAKLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CV-1997 (Rel. 35, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-0ST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 9%; Score 97; DB 1; Length 757; Similarity 23.18; Pred. No. 7.9; Conservative 35; Mismatches 74; Indels 22; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H -> ISPD (IN REF. 1).
EBEF8793C5951770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 NESRASLV---LQLMNKFSTNFISSIDGTSSDINTKELCGGARIY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP (POTENTIAL).
GTP (POTENTIAL).
GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         958 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase, Motor protein, GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 273106; CAA97444.1; -. SGD; 80003924; DNMI. InterPro; IPROJ01401; Dynamin. InterPro; IPROJ0375; Dynamin_central.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 AA; 84971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L40588; AAA99998.1; -. EMBL; X91488; CAA62769.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00410; DYNAMIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003130; GED.
Pfam; PF00350; dynamin; 2.
Pfam; PF01031; dynamin_2; 1.
```

NCB1_TaxID=4932;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation hetween the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as 10 and a 1s content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 7.9%; Score 97; DB 1; Length 958;
Local Similarity 22.7%; Pred. No. 11;
hes 58; Conservative 46; Mismatches 84; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 -IFGLKISNSLILDVKAEPIDDG-----KGLNLS----FPVTANVTVAGPIIGQIINL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             806 LVFELKLANYLVMIKKSSSKDDDEIENLILKGQELSNEFIYDTKIPQSLRDRFSGQLSNV 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 KASLDLLTAVTIETDPQTHQPVAVLGECASD-----PTSISLSLLDKHSQIINKFV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 GQHSESKDVIRHNER-QIMKEERMVKIRQELRYLINKGQISKCINYIDNEIPDLLKNNLE 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GVLTGTSESLLDNLGND---LSNVVDKL--EPVLHEGLETVDNTLKGILEKLKVDL---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 -----GVLQKSSAWQLAKQK----AQEAEKLLN------NVISKLLPTNTD 98
                                                          Fartmann B., Kramer B., Kramer W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

        DÓMAIN
        165
        185
        POLY-ASP.

        DOMAIN
        450
        453
        POLY-SER.

        SEQUENCE
        958
        AA; 108178
        MW; 335ADD152949FBCB
        CRC64;

                                                                                                                                                                                                                                                                                                                                    SGD; S0003196; VID30.
InterPro: JPR003877; SPKY.
InterPro: JPR003878; SPKY.domain.
Pfam; PF00622; SPRY: 1.
SMLRT; SM00449; SPRY: 1.
                                                                                                                                                                                                                                                                                                                EMBL; 272749; CAA96943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 NSVINTLKSTVSSLIQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              916 ENVISNTRAMUSTELLE 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
DOMAIN 165 18
DOMAIN 450 45
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

Search completed: August 6, 2002, 17:07:31

Job time: 873 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

אבר שתה / מסיים הסיים דמסים

OM protein - protein search, using sw model

August 6, 2002, 16:53:58 ; Search time 111.35 Seconds (without alignments) 386.850 Million cell updates/sec Run on:

US-10-020-139-2

1 MLQLWKLVLLCGVLTGTSES.........NVIQQVVDNPQHKTQLGTLI 249 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_vertebrate:* sp_organelle:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fung1:* sp_rodent:* sp_virus:* sp_plant:* sp_phage:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	Description	Q9bqq0 homo sapien	Q96dr5 homo sapien	P79124 bos taurus	P79125 bos taurus	Q9d734 mus musculu	Q63471 rattus norv	Q63550 rattus norv	Q96hk6 homo sapien	Q61114 mus musculu	Q9d6p2 mus musculu	Q9d794 mus musculu	Ogogx3 mus musculu	Q9d6p0 mus musculu	Q9d9j8 mus musculu	Q9bqp8 homo sapien	Q9smv6 arabidopsis
	DI	09860	Q96DR5	P79124	P79125	Q9D734	063471	063550	Q96нк6	Q61114	Q9D6P2	090794	0900x3	09060	090938	Q9BQP8	09SMV6
	DB	7	4	9	9	11	11	11	4	11	1.1	11	11	11	11	4	10
	Query Match Length DB	249	249	243	240	235	235	206	484	474	235	270	270	270	232	199	1075
ф	Query	100.0	4.66	35.8	34.1	29.0	27.3	17.2	12.9	12.2	12.0	12.0	12.0	11.8	10.7	10.5	0.6
	Score	1233	1225	442	420.5	357.5	336.5	212.5	159	150.5	148.5	148.5	148.5	145.5	132	129	110.5
	Result No.		7	ю	4	Ŋ	9	7	80	on.	10	11	12	13	14	15	16

099th0 staphylococ 005701 rattus ratt 099131 staphylococ 099138 straphylococ 099f62 xylella fas 077136 apis mellif 054436 staphylothe 096f11 lactococcus 096f11 lactococcus 090f10 tomato mosa 09110 tomato mosa 061352 mus musculu 099dp9 homo sapien 059040 methanococc 09kpm2 vibrio chol 09ktu2 caenorhabdi 09ktu2 caenorhabdi 09ktu2 caenorhabdi 09wq5 tobacco mos 09ja03 tobacco mos 09ja04 tobacco mos 061351 mus musculu 049548 mycoplasma	Ogfutt porcine rub Ogf169 mus musculu Ogf895 mycoplasma Ogn218 caenorhabdi Ogr47 vibrio chol Ogck49 pasteurella Ogfvx8 oryza sativ Og9u54 staphylococ
099TN0 005701 099R31 099R31 099R31 097R36 077136 075136 075143 0952C8 0991T0 061352 099040 061352 09040 098RWG 099RWG 099RWG 099RWG 099RWG 099RWG 099RWG	09DUT4 061769 061769 048995 09N2L8 09KS47 09CKA9 09FVX8
01199 9 10 10 10 10 10 10 10 10 10 10 10 10 10	12 11 12 16 10 10
825 473 473 666 666 666 718 152 118 1116 5210 2210 2210 387 387 488 1116 5116 5116 6116 628 628 628 628 628 628 638 638 638 638 638 638 638 638 638 63	551 2938 257 383 578 673 673 673
38888888888880000000000000000000000000	
	α
7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	338 338 344 344 35 36 36 36 36 36 36 36 36 36 36 36 36 36

ALIGNMENTS

RY; PRT; 249 AA.	17, Creat	l. 17, Last sequence update) 1. 19, Last annotation update)	(SIMILAR TO BOVINE SALIVARY PROTEIN BSP30).			Craniata; Vertebrata;	Primates; Catarrhini; Hominidae; Homo.				to the EMBL/GenBank/DDBJ databases.		Z/UII MW; E64E0/94AIB4DB/D CRC64;		100.0%; Pred. No. 2e-82; ive 0; Mismatches 0;	MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGTLEKLKV	MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV (DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG	DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG	KGLNLSPPVTANVTVAGP11GQ1INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS	KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS	
JT 1 20 09BQQO PRELIMINARY		01-JUN-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.	BA49G10.1 (SIMILAR TO		Homo sapiens (Human).		Mammalia; Eutheria; P	11)	SEQUENCE FROM N.A.		Submitted (JUN-2001)	121901: CACO	SEQUENCE 249 AA; 2		Best Local Similarity 100 Matches 249; Conservative	1 MLQLWKLVLLCGVLTG	1 MLQLWKLVLLCGVLTG	61 DLGVLQKSSAWQLAKQ	61 DLGVLQKSSAWQLAKQ	121 KGLNLSFPVTANVTVA	121 KGLNLSFPVTANVTVA	
RESULT Q9BQQ0 1D Q	AC DI	T T	E	S	SO	ဗ	88	S Z	RP.	RA	RL	DR	ÖS.	ō	M B	Qy	qq	δÿ	Dp	ΟŸ	QD	

ö

a

```
BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79413: AAB38282.1: -
SEQUENCE 243 AA: 26877 MW; OC2D8DD4560E11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 241 HKTQLQT 247
                                                                                                                                                                                                                                                                                                                                                                                            233 VTTQQES 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P79125
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                   ò
       RL
DR
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDNAs coding for alternate forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ISLSLIDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verkatesh S.G., Geetha C., Gorr S.-U.; "A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DLGVLOKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
       181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MIQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia: Pecora; Bovoidea;
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.6%; Pred. No. 7.86-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF432917; AAL28113.1; --
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AA.
                                                                                                                                 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                   PRT;
                                                                                                                                                                            (TrEMBLrel. 19,
                                                                                                                                                                                                     PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                     (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 HKTOLOTLI 249
                                      241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     TISSUE-PAROTID;
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                             01-DEC-2001
                                                                                                                                                                                         01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P79124
                                                                                                                                                    096DR5
                                                                                                                                    Q96DR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BSP30
                                                                                                           RESULT
                                                                                                                        096DR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                         ò
```

```
Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDMAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/UDBJ databases.
EMBL; U79414; AAB38283.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ISLSLLDKHSQ11NKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 E---LESRCSDEVVEQ--QETENFLEQLISRIFQVVSRLTGVRIRNVQVPDITFEATSEN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 SA-NVLIPITADVTVSLPFLGEIVDLDLNVDLQTTVSIETD--TEDPQVVVGECTNNPES 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 SA-DVSIPITADVTVSLPLLGEIVKLDLNVDLQTSVSIETDAETGDSRVVVGECPNNPES 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                   61 DIGVLQKSSAWQLAKQKAQEAEKILLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                   58 EL----ESRCLNDVVEETQQTENSLEGLISRIFQVVNRLTGVRIRNVQVPDITFEATSEN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEQEWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                   8; Gaps
                                                                                                                                                                                                1 MVQLWKLVLLCGLLAGTSESLLDIRGND---VLRRLISGLERGLGTFDST1E11FQNLKT 57
                                                                                                                                   1 MLQEWKEVLLCGVLTGTSESLLDNLGNDLSNVYDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.1%; Score 420.5; DB 6; Length 240; 38.1%; Pred. No. 3.5e-23;
35.8%; Score 442; DB 6; Length 243; 38.9%; Pred. No. 9.5e-25; Live 58; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26513 MW; 850611DE9E43E358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
```

ò

```
EMBL; M83209; AAC06334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98129760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMGB1/SMGB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 DN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 SN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q63550;
Q63550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  063550
       SO THE REPORT OF THE SOURCE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arakawa T., Hara A., Shipata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shipata K., Yoshino M., Itoh M., Ishii Y., Rawai T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Anzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radota K., Matsuda H.A., Ashburnar M., Hatalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Hatalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Hatalov S., Casavant T., Radota K., Matsuda H.A., Saburnar M., Masher G., Casavant T., Radota K., Okido T., Fesole G., Quackenbush J., Sakai K., Okido T., Furuni R., Yamashi T., Washi F., Sakai K., Okido T., Futcher C., Fujita M., Wagner L., Washio T., Butk C., Fletcher C., Fujita M., Gariboldi M., Barke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Salok K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whintaker C., Willming L., Washima K., Wangi K., Wangi K., Wawaji H., Kohtsuki S., Wangi K., Wangi K., Kawaji H., Kohtsuki S.,
170 ISLTVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDAECVEKLIGESO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 NGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGKCSSNT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSLILDVKAEPID 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 DKISISLLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSVLGGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 DVELLQQATSWPLAKNSILET --- LNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFQPGSLVVLCGLLIGNSESLLGELGSAVNN------LKILNPPSEAVPQNLNL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adyashizaki 1.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 357.5; DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24737 MW; A29D0160268DA0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Mismatches
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL: AKO09654; BAB26418.1; -
MGD: MGI:97787; Psp. -
SEQUENCE 235 AM. 24737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
                                                                       241 HKTO 244
                                                                                                                                          230 DTTQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                            Q9D734
Q9D734;
                                                                                                                                                                                                                                                     RESULT 5
Q9D734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
Q63471
ID Q63471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  063471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

g ò qq ò ΩD ò

```
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG--LKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 DVGSLQQATTWPSAKDSILET --- LNKV -- ELGNSNGFTPLNGLLLRVNKFRVLDLQAGL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 IDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 DPTSISLSULDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLQLWKLYLLCGVLTGTSESLLDNLGNDLSNVYDKLEPYLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
NEONATAL SUBMANDIBULAR GLAND PROTEIN.
0B36EC779025986E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirels L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TremBirel. 01, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY; TISSUE=SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 336.5; DB 1
31.8%; Pred. No. 4.5e-17;
tive 62; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel, 01; Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 267:2679-2687(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                MEDLINE=92129360; PubMed=1370829;
Mirels L., Ball W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330:437-444(1998).

    SIGNAL
    1
    20
    P

    CHAIN
    21
    235
    N

    SEQUENCE
    235
    AA;
    24529
    MW;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
[1]
```

proteins." Mirels L.,

Query Match

QQ ò

CHAIN

.. 5

40;

```
102 TYNQELVVRIPLDMVAGLNTPLIKTIVEFQMSTEVQALIRVERSKS--GPAHLNLSDCSS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 DDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAV-LGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 LKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 LPL-LRAMQDKSG-----SIPILDSFVHTVLKY---IIWMKVTSANILQLDVQPS 101
                                                                                                                                                                                                                                                                                                                                   173 ECASDPTSISLSLDRKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLJVNVI 232
                                                                                                                                                                                                                 117 IDDGKGLNLSFPVTANVTVAG---PIIGQIINLKASLDLLTAVTIFTDPQTHOPV-AVIA 172
                                                                                                                                                                                                                                                              102 SANDOELLVKIPLD----MVAGENTPLVKTIVEFHMTTE--AQATIKMDTSASGPTKLVLS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 WKLVLLCGVLTGT-----SESLLDNLGNDLSNVVDKLEPVLHFGLETVDNTLKGILEK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 WILTLICGLIGATIVQANVYPPAVL-NIGPEV-----IQKHLTQALKDHDAT--ATLQE 55
                                                                                                                             63 -----GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                      45 KDHNATSILQQLPLLSAMREKPAGGIPVLGSLVNTVL---KHVJWLKVJTANIJQLVVKP 101
                                      5 WKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKLKVDL 62
                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%: Score 150.5; DB 11; Length 474: nilarity 23.1%; Pred. No. 0.004; Conservative 56; Mismatches 84; Indels 33;
97; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 NESTLRISLLHKISFVVNSLAKNVMNLLVPALPQIVKNHLCPMIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VON EDNER MINOR SALIVARY GLAND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 474 AA.
Matches 58; Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SWISS-WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                        233 QQV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 QLV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9D6P2
Q9D6P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q61114
Q61114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9D6P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                         δŏ
                                                                                                                                                                                    q
                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 IDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SPNGDEVTLKMPMALNASLSLPARDLTTDVSISMEAITSFAIEKDPKTGRRVLNMQRCSL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 DPTSISLSLEDKHSQIINKFVNSVINTLKSTVSŞLLQKEICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 NTDNTSISLLNRKSNEVNLALDSALYLIKRGLTLPVRRQLCPVLQLIISN---TFHPDEI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein multigene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KRGIE-----LKIKDLRILNLNHEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLQLWKLVLLCGVLTGTSESLLDNLGN---DLSNVVDKLEPVLHEGLETVD-NTLKGILE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFQLGSLVVLCGLL1GTSGSLFDIFQNPELDVESVWSEINYRIRYALETMDLDMLADYLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
NEONATAL SUBMANDIBULAR GLAND PROACINAR
CELL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelcostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 206;
                                                                                                                                                                                                                                                                                 Americals L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%; Score 159; DB 4; Length 484; 23.9%; Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLIEL 19, Created)
01-DEC-2001 (TrEMBLIEL 19, Last sequence update)
01-DEC-2001 (TrEMBLIEL 19, Last annotation update)
SIMILAR TO DNA SEGMENT, CHR 2, MASSACHUSETTS INSTITUTE OF
TECHNOLOGY 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO08429; AAHO8429.1; -
SEQUENCE 484 AA; 52427 MW; 08242B697284E858 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 206 AA; 23027 MW; 91C001620761067B CRC64;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN*SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE=98129760;
                              STRAIN-SPRAGUE-DAMLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-92129360; PubMed~1370829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 212.5; DB 1 24.2%; Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 24.2%; Pred. No. 4.2e-
Matches 59; Conservative 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKT;
                                                                                                                                                                      Biol. Chem. 267:2679-2687(1992).
                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 330:437-444(1998).
                                                                                                                                                                                                                                                                                                                                                                         EMBL; M83210; AAC12783.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                      20
206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 DNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 SNPQ 201
```

33; Gaps

Query Match

096HK6

RESULT Q96HK6

q

δ

```
STRAIN-C57BL/6J; TISSUE-TONGUE;

RX MEDLINE-21085660; PubMed=11217851;

RA Arakwa T.; Shinagawa A.; Shibata K.; Yoshino M., Itoh M., Ishii Y.;

Rawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;

Rawai J.; Shinagawa A.; Pikhata K.; Konno H.; Adachi J.; Fukuda S.;

Radawa K.; Izawa M.; Nishi K.; Konoo S.; Yamanaka I.;

RA Alzawa K.; Izawa M.; Nishi K.; Yoshino H.; Kando S.; Yamanaka I.;

RA Alzawa K.; Izawa M.; Nishi K.; Goodoo S.; Yamanaka I.;

RA Alzawa K.; Cojobori T.; Bono H.; Kashawa T.; Salto R.;

RA Alzawa K.; Matsuda H.; Baralov S.; Casavant T.;

Radia P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.;

Radia P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.;

Robinial L.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.;

Radia J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.;

Radia J.; Boffelli D.; Hofmann M.; Hume D.A.; Kamiya M.; Lee N.H.;

Ruchone P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.;

Ruchone P.; Ring B.; Ringwald M.; Rodriquez I.; Sakamoto N.;

Rusaki H.; Toyo-oka K.; Wang K.H.; Weitz C.; Whittaker C.; Wilming L.;

Marshi, A.; Voshida K.; Hasegawa Y.; Rawaji H.; Kohtsuki S.;

Marshi, A.; Voshida K.; Hasegawa Y.; Rawaji H.; Kohtsuki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 VLGKVISS-1PLLNNILDIRVINPQLLEIGLVOSYDFHRLYVTIPLGFDLRVNTLVVGSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1919687; 2310074B19Rik.
ENCE 235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                    17, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.0%; Score 148.5; DB 25.3%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 LKSTVSSLLQKEICPLIRLFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=TONGUE; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK010143; BAB26728.1; -
01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2310021H06RIK PROTEIN.
2310021H06RIK.
                                                                  2310074B19RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                        2310074B19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
RA Arzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radota K., Matsuda H.A., Rabburner M., Batalov S., Casavant T., RA Ardota K., Matsuda H.A., Gissi C., King B., Kochiwa H., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quadkenbush J., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N., RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Rawashinaki V., Kawaji H., Kohtsuki S., Anarashinaki V., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C55BL/6J; TISSUE-TONGUE;

X MEDLINE=21085660; PubMed-11217851;

XA Arawia J. Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arawara T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawawa T., Shinaqawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

RA Arawawa T., Samanaka I.,

RA Alzawa K. Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Isawa M., Nishi K., Shiosawa H., Kasukawa T., Saito R.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fleicher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fleicher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Humez D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 VLGKVISS-IPLENNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
κ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 148.5; DB 11; Lenyun. 25.3%; Pred. No. 0.0028; Lidels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA; 29223 MW; DB63327561D910AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel, 17, Created)
01-JUN-2001 (TrEMBLrel, 17, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK009441; BAB26290.1; -.
MGD; MGI:1914385; 2310021H06Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310021H06R1K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09C0X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09CQX3
```

φ

```
ABLANKA-CSTBL/61, TISSUE-TONGUE;

XX Rawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Rawai T., Hara A., Fubunishi Y., Konno H., Adachi J., Fukuda S.,

Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Saito T., Okazaki Y., Golobori T., Bono H., Kasikawa T., Saito R.,

XA Saito T., Matsuda H.A., Ashburner M., Batalov S., Caswant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caswant T.,

XA Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XA Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Blake J., Boffelli D., Holmann M., Hume D. A., Kamiya M., Lee N.H.,

Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Bordonselm M.J., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Buzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Mynshwa-Boris A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S.,

A Havaening H.
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 INEKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ILUNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLON-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection.";
                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492A16EEBAB4A677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.0%; Score 148.5; DB 25.3%; Pred. No. 0.0028; tive 38; Mismatches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AK010051; BAB26667.1; --
MGD; MOT:1914485; 2310021H066Rik.
SEQUENCE 270 AA; 29175 MW. **
                                                                                                                                                                             EMBL, AK010115; BAB26710.1; EMBL; AK009329; BAB26221.1; EMBL; AK009531; BAB26343.1;
                                                                                                                                                                                                                                                                                                                         AK009580; BAB26372.1; -. AK009629; BAH26401.1; -. AK009695; BAH26444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK010012; HAB26642.1; -. AK010051; BAB26667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AK009803; BAB26513.1; -.
                                                                                                                                                                                                                                                                                           AK009562; BAB26360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK009835; BAB26533.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                   Nature 409:685-690(2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2310021H06RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D6P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO OR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C55BL/61: TISSUE-TESTIS;

K STRAIN-C55BL/61: TISSUE-TESTIS;

K Kawai J., Shinagawa A., Shibata K., Koohino M., Itoh M., Ishii Y.,

K Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Kadohi J., Fukuda S.,

R Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

R Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

R Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Robill D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

R Chrimi L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

R Hake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Hake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Hownstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M.,

R Jyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

R Haysakii R., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayasakii A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 84 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGGI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 LELSVKLDVTAEVYAVRDFYGRSRL-VIGDCIYPPGSLKISLLNRLGPLON-LIDSUTUI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LWK-LVLLCGVLT-----GTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LWRLLVLLLGLLALPSALPKQPWPGLTKAHKDGRST-----LARIIAQGLLKLN--A 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 132; DB 11; Length 232; 21.1%; Pred. No. 0.036; tive 54; Mismatches 88; Indels 64
                                                                                                                                                                                                                                                 Match 11.8%; Score 145.5; DB 11; Length Local Similarity 25.3%; Pred. No. 0.0046; Les 39; Conservative 38; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AA; 25713 MW; 0D52D24A3076D5DC CRC64;
Nature 409:685-690(2001).
EMBL: AK010145; BAB26730.1J. -.
MGD: MGI:1914385; 2310021H06R!k.
SEQUENCE 270 AA; 29235 MW; A86F02ABBAAFBCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 LTRVIPGLVQGVVCPLVNGVLSLLDV″LAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK006829; BAB24760.1; -.
MGD; MGI:1920638; 1700058C13Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700058C13RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
"...os 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1700058C13RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090938;
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOCCOON THE SECTION OF SECTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

52 KG-----ILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 105

```
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 -----GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 IDDGKGLNLSFPVTANVTVAG----PIIGQIINLKASLDLLTAVTIETDPQTHQPV-AVLG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 KDHNATSILQQLPLLSAMREKPAGGIPVLGSLVNTVL.---KHIIWLKVITANILQLQVKP 101
                                                                                                               106 NSLILDVKAEPIDDGKGLNLSFP···VTANVTVAG-···-PIIGQIINLKASLDLLTAV 156
                                                                                                                                                                           102 ------DCGGIQMAFPKEWFSANITLEFDIEFKLPFNSNIKTHACMGLTAES 148
                                                                                                                                                                                                                                                                                                    157 TIETDPQTHQPVAVIGECASDPTS(SLSL-LDKHSQIINKFVNSVINTLKSTVSSLLQKE 215
                                                                                                                                                                                                                                                                                                                                                            149 WLEKDEFGRREL-VMGRCRMEPSSGGASMSTEETSPKMKHFLHNLRESLGKVIPNLVESQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.5%; Score 129; DB 4; Length 199; Best Local Similarity 24.2%; Pred. No. 0.049; Matches 54; Conservative 40; Mismatches 89; Indels 40; Gaps
54 ECRIQSMRLLDRLNVSGTVAPGMVGWLIGGMNFQQQQEISINI-----TNVQL----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S WIFTLEGELAATE------IQATESPTAVILG------PKVIKEKLTQEE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 WKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKLKVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49G10.6 (SIMILAR TO MURINE VON BENER MINOR SALIVARY GLAND PROTEIN, ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracey A.; submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001); CAC03550.1; -. NON_TER 1199 199 AA; 21517 MW; 49A4CC2143BE04B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 ECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||: || :: || :: || || :: || || :: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 ICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||| : ||| ::::|
208 VCPLIGEILRQLDVKLLKGLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DJ1187J4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BQP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
Q9BQP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ολ
```

Search completed: August 6, 2002, 17:09:28 Job time: 930 sec

```
(without alignments)
199.620 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SIDSI/gggdata/hold*geneseqy/geneseqy=embl/AAJ991_DAT:
| SIDSI/gggdata/hold*geneseqy/geneseqy=embl/AAJ991_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAJ992_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAJ992_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAJ992_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAJ996_DAT:
| SIDSI/gggdata/hold*geneseqy=geneseqy=embl/AAJ996_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAJ998_DAT:
| SIDSI/gggdata/hold*geneseqy=embl/AAZ9000_DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1982.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseg/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegy-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-genesegy/genesegp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLQLWKLVLLCGVLTGTSES.....NVIQQVVDNPQHKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                  August 6, 2002, 16:47:18 ; Search time 138.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                               OM protein . protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-020-139-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		fumer parotid secr	Human parotid secr	Human PROIDES prot	Human secreted pro	Human secreted pro	Human protein segu	repulde #8941 enco	Human brain expres	Human bone marrow	Peptide #9264 enco Mouse 28.6 kDa sec	
SUMMARIES	QI	AAW69221	AAW60682	AAB24069	AAB25765	AAB75351	AAM25745	ABB41435	AAM6230B	AAM75111	AAM35227	AAE05367	
	DB	19	19	21	21	22	22	22	22	22	22	22	
	Query Match Length DB ID	249	249	249	249	249	260	20	50	50	50	278	
dю	Query Match	100.0	100.0	100.0	100.0	100.0	6.96	20.0	20.0	20.0	20.0	15.5	
	Score	1233	1233	1233	1233	1233	1195	246	246	246	246	191.5	
	Result No.	-	7	æ	4	S	9	7	œ	o,	10	11	

Human secreted pro LS170 polypeptide Amino acid sequenc Human secreted pro Human PRO polypept Human polypeptide	Human LUNX protein Human digestive sy Human polypeptide Human digestive sy Human digestive sy Human NOV6a protei	Human NOV6b protei Human neurotransmi Novel human diagno Amino acid sequenc Human PRO1357 (UNO Human PRO polypept Human PRO polypept	rotein of the i uman secreted p ung cancer asso taphylococcus a taphylococcus a difficile tox lostridium diff	Staphylococcus aur Staphylococcus aur Recombinant endoto Recombinant endoto Amino acid sequenc Human KSP. Homo s Haemophilus influe Human secreted pro
AAYO6 AAW95 AAY69 AAU39 AAM39	AAB9736 AAM9220 AAM4150 AAM9221 AAM9721 AAM4721		乙1737180	AAU370 AAW168 AAW168 AAG674 AAB472 AAU355
999999	544710	০ কৈ তা ক ক ক ক	484 2 197 2 221 221 2 221 2 221 2 2710 1 2710 1 2025 2 2025 2 2025 2 2	158 158 481 057 057 210
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	12.9 12.9 12.8 12.8	21 21 20 20 20 20 20 20 20 20 20 20 20 20 20	888888888888888888888888888888888888888
	93. 16 16	160 159 158 158	158 122 108 108 104 104	102 101 101 100 100 99
12 13 14 15 17	7	200 200 300 300 300	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	W44444 WOH4W4W

ALIGNMENTS

```
Parotid secretory protein; hpsp. digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                                                                                                /note= "signal peptide"
                                                                                                                                                                          19.249
/note= "mature hPSP"
                 AAW69221 standard; Protein; 249 AA.
                                                                                                                                                  Location/Qualifiers
                                                                       Human parotid secretory protein.
                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                           97WO-US23522.
                                                                                                                                                                                                                                                             96US-0034429.
                                                   16-OCT-1998 (first entry)
                                                                                                            therapy: diagnosis,
                                                                                                                                                                                                                                                                                               Duan R, Ruben SM;
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                           23-DEC-1996;
                                                                                                                                                                                                    WO9828420-A1
                                                                                                                                                                                                                                          18-DEC-1997;
                                                                                                                                                                                                                       02-JUL-1998
                                    AAW69221;
                                                                                                                                                        Peptide
                                                                                                                                                                           Protein
        AAW69221
RESULT
```

us-10-020-139-2.rag

```
AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρp
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                      Interaction. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting).

Consider the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting).

Consider the corresponding genomic DNA. The DNA and protein can be maplification or immuno assays), particularly for diagnosis of diagnosis of cancers of the saltwary gland, thymus and paperceas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibecterial, antiperasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific antigonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated in the excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parotid secretory protein; human; cancer; autoimmune disease; secretory lissue; gastrointestinal tissue; HSPSP, Sjorgen's syndrome; Graves disease; thyroidilis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 dlgvlqkssawqlakgkaqeaekllnnviskllptntdifglkisnslildvkaepiddg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 mlglwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkv 60
                                                                                                                                               This sequence is the human parotid secretory protein (hPSP) of the
                                              New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 1233; DB 19; Length 249; Best Local Similarity 100.0%; Pred. No. 1.2e-100; Malches 249; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW60682 standard; Protein; 249 AA.
                                                                                                               Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                hPSP-binding proteins.
WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 hktglqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA;
                   N-PSDB; AAV44759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09821329-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW60682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DLGVLQKSSAWQLAKOKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KGLNLSFPVTANVTVAGPLIGQIJNLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNV1QQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKG1LEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect that express HPSP, to monitor patients being treated with HPSP, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 1233; DB 19; Length 249; Local Similarity 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB24069 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-C; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                97WO-US20651.
                                                                                                                                     96US-0749288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2001 (first entry)
                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal tissues
                                                                                                                                                                                                                                                                   Bandman O, Goli SK;
                                                                                                                                                                                                                                                                                                                                 WPI; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 hktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV37699.
                                                                07-NOV-1997;
                                                                                                                                 14-NOV-1996;
22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

ö

1 MLQLWKI,VLI,CGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKG1LEKLKV 60

```
PRO genes. Exemplary conditions or disorders to be treated with supplicing antibodies and other compounds include benign or malignant tumours colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other qlandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC5816 represent por primers and hybridisation probes used in the isolation of the human prosequences. AAC5836 to AAC5836 represent properties. AAC5836 to AAC5836 represent manner properties. AAC5806 of the human properties and hybridisation probes used in the isolation of the human properties. AAC5806 to AAC5806 represent human properties and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO311, PRO535, PRO6199, PRO317, PRO809, PRO319, PRO8197, PRO1009, PRO1009, PRO1005, PRO1009, PRO1005, PRO1009, PRO1005, PRO1009, PRO1005, PRO1009, PRO1005, PRO1009, PRO1005, PRO1009, PRO2009, PRO2005, PRO319, PRO2005, PRO319, PRO2005, PRO319, PRO2005, PRO319, PRO2005, PRO319, PRO2005, PRO319, PRO3190, PRO3190
                                                                             Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; neotropic; neuroprotective; antiinflammatory; immunosuppressive; immunosimulant; antianquogenic; leukaemia; lymphoid malignancy; neuronal disorder; glaid disorder; astrocytal disorder; angiogenic; hypothalamic disorder; qlandular disorder; macrophagal disorder; inflammatory disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis and prevention of cancer
                          Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US12252.
99US-0141037.
99US-0143048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145698.
99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2000; 2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                         WC200053755-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
```

ROY MA;

```
Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alabeimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAARY125-AB774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequence data on a computer system, and a method for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted
                     181 islslldkhsginkfvnsvintlkstvssllgkeicplirifihllllllllllll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                         121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                   181 ISLSELDKHSOIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bougueleret L., Dumas J., Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                            AAB25765 standard; Protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113686.
99US-0141032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-1B02058
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442637/38.
                                                                                                                                                                                                                          241 HKTQLQTL1 249
                                                                                                                                                                                                                                                              241 hktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA87727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200037491-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000
                                                                                                                                                                                         g
                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                     a
                                                                             ó
                                                                                                             q
                                                                                                                                                   ò
```

Gaps

: 0

Indels

..

0; Mismatches

Best Local Similarity 100. Matches 249; Conservative

Query Match

100.0%; Score 1233; DB 21; Length 249; 100.0%; Pred. No. 1.2e-100;

us-10-020-139-2.rag

ó

```
8 × 6 6 6 6
                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                    181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                      61 DLGVLOKSSAWOLAKOKAOFAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                             121 kglnlsfpvtanvtvagpiigqiinlkasldlltavtietdpqthqpvavlgecasdpts 180
                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                     1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49\ Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -
                                                                                                                                                         100.0%; Score 1233; DB 21; Length 249; 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bougueleret L, Jobert S;
                                                                                                                                                                                 0
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2000; 2000WO-IB00951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0141032.
99US-0469099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001 (first entry)
                                                                                                                                                                                 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-071487/08.
                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                           241 hktqlqtli 249
                                                                                                                      249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JAN-2001.
                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB75351;
                                                                                                                                                           Query Match
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75351
  5555555555558888
                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
```

```
antlinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antialstatic; untiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulant, gene therapy, antisense therapy; vaccine, inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ULGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIQIMKLVILCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disease; haematopoietic disorder; platelet disorder; asthma;
The present invention relates to 49 Secreted proteins and the CDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopaenia, osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                              100.0%; Score 1233; DB 22; Length 249; 100.0%; Pred. No. 1.2e-100;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                        ..
O
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ 1D NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0471275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                    Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder.
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 hktqlqtli 249
                                                                                                                                                                       249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM25745;
                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM25745
```

```
AAM62308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
 AAM99166, to AAH99904 encode the human proteins given in AAM25225 to
AAM26363. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinflammatory; antinheumatic;
antiatrhritus; immunosuppressive; antibacterial; endocrine; cardiant;
central nervous system; virucide; anti-HVV; fungicide; antimutagen;
antidiabelic; oftendatological; antiallergic; antiasthmatic;
antidiabelic; oftendatic; neuroprotective; antidepressant; nootropic;
antidiabelic; softendatic; neuroprotective; antidepressant; nootropic;
antidiabelic; special and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis, of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                           anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczemia, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ISLSLLDKHSQIINKFVNSVINTLKSTVSSILQKEICPLIRIFIHSI,DVNVIQQVVDNPQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 dlgvlqkssawqlakqkaqeaekllnnviskllptntdifglkisnslildvkaepiddg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHOPVAVLGECASDPTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLQLWKIVLLCGVLTGTSESILDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                              Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 mlglwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkv 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.9%, Score 1195, DB 22; Length 260; 97.2%; Pred. No. 2.7e-97;
Live 1; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                              Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB41435 standard; Peptide; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.2
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disorders.
                               2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 HKTQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 hktglqtli 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA;
Tanky YT, Liu C,
                                                 N-PSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB41435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
ABB41435
δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.2e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 piigqiinlkasldlltavtietdpqthqpvavlgecasdptsislslld 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM62308 standard; Protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                          2000US -0180312.
                                                                                                                                                                                                                                                                             2000US-0608408
                                                                                                                                                                                                                                                                                                                                               21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                    30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                              03-AUG-2000; 2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer.
W0200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                             30-JUN-2000;
                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM62308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

9

```
probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leuksemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #9264 encoded by probe for measuring placental gene expression.
                                                      The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                          0;
                  Example 4; SEQ ID NO: 35417; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                   20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                138 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%; Score 246; DB 22; Length 50;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ 1D No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Kank DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                       20.0-
100.0%; Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM35227 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-0CT-2001 (first entry)
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                             50 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM35227;
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM35227
                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded protein SEQ 1D NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                     Example 4; SEQ 1D NO: 34413; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 246; DB 22; Length 50; 100.0%; Pred, No. 1.2e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 PIIGOIINLKASLDLL/TAVTIETDPOTHOPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM75111 standard; Protein; 50
                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                   2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                           the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0236359
                  2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53
                                                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
03-AUG-2000;
                  21-SEP-2000;
                                   27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM75111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM75111
```

```
treatment of mammalian diseases which is the properties of inappropriate of an appropriate of treatment, and as a serior properties of the differentiation of tissue specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or cher compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of are useful in genome and physical mapping, in positional cloning of treatment of mammalian diseases which is the consequence of inappropriate corresponding immune response or treatment of an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of an immunoregulatory and anti-inflammatory molecule, as a part of a vaccine or anti-cancer treatment, as immunoregulatory and anti-inflammatory molecule, as atti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit to remain the material manner of the invention, for tissue and neural regeneration, to promote or block the invention, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant.
                                          0
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse, cytostatic; antlinflammatory; immunoregulatory; tissue integrity; wound healing; immune response; vaccine; cancer; asthma; allergy; cell trafficking; therapy; 28.6 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses novel polynucleotides and their corresponding
                                          .;
0
                                                                                  138 PIIGQIINEKASLDELTAVTIETDIVQTHQPVAVEGECASDPTSISESED 187
                                                                                                         1 piiggiinlkasldlltavtietdpqthqpvavlgecasdptsislslld 50
Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                          AAE05367 standard; Protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 92; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Mouse 28.6 kDa secreted protein.
                     100.0%; P.
Live 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-2000; 2000US-0724864
                                                                                                                                                                                                                                                                                                                                 12-SEP-2001 (first entry)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watson JD, Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-425665/45.
                     Lecal Similarity
les 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD10135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                          Matches
```

```
61 spalpsnptdllagkftdalsgql-----lsggl-----lgileniplldviksgggn 108
                                                                                                                                                                                                        81 AEKLLNNVISKL---LPTNTD[FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG 137
                                                                                                                                                                                                                                   109 snglvggllgkltssvpllnnildikitdpgllelglvgspdghrlyvtiplgltlnvnm 168
                                                                                                                                                                                                                                                                        138 PIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLLDKHSQIINK 195
                                                                                                                                                                                                                                                                                                         169 pvvgsllglavklnitaevlavkdnggrih---lvlgdcthspgslkisllngvtp-vgs 224
                                                                                                      l mflvgslvvlcgllahstaqlaqlplplgqgpplplnqgpplplnqgqllplaqglplav 60
                                                                                                                                        30 ----SNVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a novel human secreted protein, termed hit796_1. The sequence is predicted from a full-length CDNA clone (see AAX59356) isolated from a human adult brain (thalamus) cDNA library. The invention provides cDNA clones (see AAX59352-58)
                                   61;
     DB 22; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; nh796_1; human; brain; thalamus; therapy;
                                                                                                                                                                                                                                                                                                                                                              |:::: | : |:| ::||| 225 fldnltgiltkvlpeliggkvcplvngilsgldvtlvhniaellihglq 273
                                                                                                                                                                                                                                                                                                                                           196 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
 15.5%; Score 191.5; DB 22; Length 23.2%; Pred. No. 7.4e-09; Live 50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "predicted leader/signal sequence"
                                                                       1 MLQLWKLVLLCGVLTGTSESLLD------NLGNDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K, LaVallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg D, Steininger RJ, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY06408 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0222653.
98US-0070346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US27903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
Ouery Match
Best Local Similarity 23.2%
Matches 67, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-419350/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX59356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9935252-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                       qq
                                                                                                                                        ó
                                                                                                                                                                        a
                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                           ò
```

```
75 KOKAQEAEKLLNNVISK---ILPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                   78 kpgggtsggilggllgkvtsvipglnniidikvtdpgllelglvgspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 NVTVAGPLIG-QTINNLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 kigyntpivgasilriavkiditaeilavrükgerihl-vigdcthspysigisilögig 196
encoding novel secreted proteins (see AAY06404-10) of the human tests, brain and foetal kiddey. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell provided. Suggested activities include nutritional, cytokine, cell vaccine) or immunosuppressive, haematopoiesis regulating, tissue sprowth, activin or inhibin, chemotactic or chemokinetic, hammosuppressive, haematopoiesis regulating, tissue haemostatic, thrombolytic, receptor/ligand, antiinflammatory, cadherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                                         Mismatches 100; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                    15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLGVLGKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                                                    45 tglagsitnaisngl-----isggl----igilenlplidil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ES170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 Q1-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 plpigglldsltgilnkvlpelvggnvcplvnevlrglditlyhdivnmlihylg 251
                                                                                                                                                                                                                                                                       14.9%; Score 183.5; DB 20; Length 256; 23.8%; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New 5,5170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;
Roberts-rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colpitts TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US11601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0049183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSi70 polypeptide sequence.
                                                                                                                                                                                                                                                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Granadosen,
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                         256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-060335/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Billing-medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX00809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9856951-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998.
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95463;
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95463
     8x36666666668x8
                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Sequences AAW95463-47] represent LSI70 polypeptide fragments which contain at least on epitope in their sequences. The present invention contain at least on epitope in their sequences. The present invention treating a test sample with at least one LSI70 specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) and the are fragments derived from various clones of LSI70 gene. The LSI70 coulding acid fragments represent a set of configuous, partially contained in a sequences (AAX00801-09) and disease. Specifically cancer, and to indicate predisposition to such disease. Particularly detection of LSI70 polynucleotide. ISI70 antibodies is indicative of disease. Cells cantigened with an expression system comprising the LSI70 nucleic acid are used to express recombinant polypeptides. The polypeptides can be used to raise Ab and for drug screening. LSI70 related nucleic acid are says. as targets for drug screening. LSI70 related nucleic acid assays; as targets for drug screening, and as components or largets for the many, e.g. as antisense, ribozyme or triplex.forming apents in the contains and reagents in the largets.
                                                                                                                                                                                                                                                                                                                                                           therapy, e.g. as antisense, ribbzyme for triplax-forming agents, lower therapeutic agents to LS170-expressing cells; directly competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 KUKAQEAEKILUNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 kpgggtsggliggligkvtsvipglmniidikvtdpqlleiglvgspdghrlyvliplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 NVTVAGPIIG-QIINLKASLDI.LTAYTIETDPOTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 kiqvntplygaslirlavkiditaeilavrdkqerihl-vigdcthspgsiqislidgig 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 tglagsltnalsngl-----lsggl-----lgilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 OI-INKFVNSVINTLKSTVSSLLQKEICPLFRIF1HSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 197 | Pipiqquldaltqilnkvlpelvqgnvcplvnevlrglditlvhdivnmlihqiq 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%; Score 183.5; DB 20; Length 256; 23.8%; Pred. No. 3.4e-08; tive 46; Mismatches 100; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sun Y, Recipon H, Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69164 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0095233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DIAD-) DIADEXUS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200008206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY69164
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
```

```
Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; voytostatic; antidiabetic; viruode; antiinfertility; anticonvulsant; antirheumatic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; pardiodontal disease; mytoloid deficiency; wound healing; ulcer; periodontal disease; mytoloid deficiency; wound healing; ulcer; parkinson's disease; Hunthagton's disease; infection; caldiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                     Lung specific genes for developing products for diagnosing, monitoring, staging, prognosticating, imaging and treating lung cancer
                                                                                                                                                                                                                                                                                                                                                The present sequence is encoded by a lung specific gene, designated Lug110, clone ID 1355520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer. Sepecially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 klqvntplvgasllrlavklditaeilavrdkgerihl-vlgdcthspgslqislldglg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 KOKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches 100; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 tglagsltnalsngl----lsggl----lsggl----lgilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNV1QQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.9%; Score 183.5; DB 21; Length 256; Best Local Similarity 23.8%; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                            Example 2; Page 35-36; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU39019 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          food supplement; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating lung cancer.
                                      WPI; 2000-195589/17.
                                                                                N-PSDB; AAZ61165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175068-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU39019
XXX AAU39019
XXX XXX AAU3
XX XX Human
DJT 16-JJ
XXX Human
XXX Human
XXX Human
XXX Human
XXX AAU3
XXX HUMAN
XXX AAU3
XXX HUMAN
XXX
D
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
Db
```

```
impunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoparthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, anylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, infarction of cardiac and central nervous system vessel e.g. stroke, septim activin- or inhibin related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in the manmals and decrease spermatogenesis in male ammunals and decrease spermatogenesis in manmals. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 kpgggtsggllggllgkvtsvipglnnildikvtdpqllelglvgspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 KQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 131
                                                                                                                                                                                                                                                                                                                                                             Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches 100; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 TGTSESLIDNLGNDLSNVVDKIJEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 tglagsltnalsngl------lsggl------1gilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lavallie E, Collins-racie LA, Evans C;
J, Steininger RJ, Spaulding V, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 183.5; DB 2 23.8%; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 497-498; 619pp; English.
                                                                                                                                                                                                                                        Merberg D;
                                                                   30-MAR-2000; 2000US-0539330.
                                                                                             04-DEC-2000; 2000US-0729674.
                    22-MAR-2001; 2001WO-US09369
                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                                                       Jacobs K, McCoy JM, La
Preacy M, Agostino MJ,
                                                                                                                                                                                                                                      Fechtel K,
                                                                                                                                                                                                                                                                                       WPI; 2001-639363/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AA;
                                                                                                                                                                                                                                                                                                              N-PSDB; AAS59237
                                                                                                                                                                                                                                        Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

9

Search completed: August 6, 2002, 16:52:51 Job time: 333 sec

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                            OM protein - protein search, using sw model
```

(without alignments) 358.294 Million cell updates/sec August 6, 2002, 17:05:10 ; Search time 66.51 Seconds Run on:

US-10-020-139-2_COPY_22249 Title: Perfect score:

1 LQLWKLVLLCGVLTGTSESL.....NVIQQVVDNPQHKTQLQTL1 248 Seguence:

Scoring table:

283138 seqs, 96089334 residues Gapup 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	, g	rotid secr	dibular	tin 1 [valid	(XPO1)	probable membrane	etical pro	os	probable ligand-bi	myosin-like coiled	cytadherence-acces	toxin A - Clostrid	hypothetical prote		eina	_	ž	hypothetical prote		biliary glycoprote	hypothetical prote	hypothetical prote	dynamin-related pr	hypothetical prote	hoseri	hetical	inva	iry qlycc	face membr
SOFFICE	ΠD		B42337	A42337	T52638	T51557 ·	.S53378	B89944	A49943	S17448	T50073	G64242	A37052	F90067	G02157	C82759	868553	D64182	B86807	WMTM8T	33	8	T27045	7	6424	8208	9097	582	C150	C600
	DB	7	a	~	C)	7	~	~	7	7	7	7	N	7	-	7	7	7	7	_	C1	~	71	-	~	N	N	~	7	7
	Length	23			0		76			47		61	71	296		9		67		61								99		
æ	Query	29.3		ė.				-				•	•	8	•	•														
	Score	59	331.5	07	10	20	109	108	~	104.5	04	104	104	103.5	8	100	99.5	9		98.5		97.5	~	97		96.5	9	9	96	96
	Result No.		7	٣	4	2	9	7	80	σ	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

> qq δλ

3 QLGSLVVLCGLLIGNSESLLGELGSAVNN------LKILNPPSEAVPQNLNLDV 50 2.QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61

Query Match 29.3%; Score 359.5; DB 1; Length 235; Best Local Similarity 33.6%; Pred. No. 4.2e-19; Matches 80; Conservative 62; Mismatches 79; Indels 17; Gaps

hypothetical protectal protectal proliferation probable DNA topoinmethyl accepting chypothetical protectonserved hypothetical protectonserved hypothetical protecton itrogenase (EC 1. ketol.acid reducto hypothetical protecton hypothetical protecton hypothetical protecton nitrogenase (EC 1. ketol.acid reducto hypothetical protecton hypothetical hypothetical protecton hypothetical hypothe	STNIS	VLT 1 Substitution of the most abundant protein in the parotid gland. Its function is necessary protein precursor - mouse leterate names: PSP pecies was musculus (house mouse) Pecies in the mescribus (house mouse) Coession: A23031; I55236 adsen, H.O.: Hinth, J.P. AA3031; MUID:85215456 A23031; MUID:85215456 AB3031; MUID:85215456 AB3031; MUID:85215456 AB3031; MUID:8704556 AB3031; MUID:8704564 AB3031; MUID:8704610 AB3031; MUID:8
42 42 42 43 43 43 43 43 43 43 43 43 43 43 43 43	ALIGNMENTS	- mouse on 31-De on 31-De 15456 15456 15456 om GB/EB 2200556; protein us predi
A64465 7304665 73080 882204 7119148 7119148 7119148 7119149 711918 71918 7	Æ	cursor - mouse e mouse) Levision 31-D 1985 mouse PSP mRN UID:85215456 in Mikkelsen, B ne parotid sec UID:87004556 ated from GB/E in NID:9200556; undant protein liva e intomplete e incomplete e gry protein liva e fstatus pred
		precursor nouse mouse mouse mouse mouse mouse for frequency of mouse; MUID:85 mile par mile mile mile mile mile mile mile mile
2005 2038 2558 1130 6713 1729 1729 462 1729 1729 1038 1038 1038		protein precursor - mouse culus (house mouse) 8 #sequence_revision 31-b6 153236
00000000000000000000000000000000000000		y protein ssculus (h 988 #seque 331; I532 331; I532 11: I532 AAD> AD> AD> GB:XOI Seb: CB:XOI FS (F) FS (F)
Q QQ QQQQ R 44 WEWE Q QQQQQ QQ Q NQQQQ QQ Q NQQQQ QQ		Parotid secretory protein precursor - mou Nalternate names: PSP (Nalternate names))))))))
0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 SOMS Parotid secre NATErnate n C, Species: Mu C, Date: 31-De C, Accession: R, Madsen, H.O R, Cross refer A, Cross refer C, Comment: PS C, Genetics: A, Gene: PS C, Genetics: A, Ann Positio A, Introns: 41, A, Introns: 41, A, Introns: 41, C, Superfamily C, Kcywords: P F; 1-20/Domain F; 1-20/Domain

```
A.Description: functions as nuclear export receptor for proteins carrying leucine-rid C.Superfamily: Arabidopsis thaliana exportin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R Haasen, D.; Koehler, C.; Neuhaus, G.; Merkle, T. Plant J. 201, 695-705, 1999
Plant J. 201, 695-705, 1999
A.F.Itle: Nuclear export of proteins in plants: AtXPOl is the export receptor for leuch A.Reference number: 226149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                    83 NGDEVTLKMPMALNASLSLPAKDLTTUVSISMEAITSFAIEKDPKTGRRVLNMQRCSLNT 142
                                                                                                                                                                                                                                                                                                                                                                                       58 KVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                  178 TSISLSLLDKHSQ1INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 VDLGVLQVLQVSSA-----W-QLAKQKAQEAEKLLNNVISK----LLIPTNTD-----1FGLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 DGKGLNLSFPVTANVTVAGP11GQ11NLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 RD-EYLORLMALPNOKWAEIIGQARHSVEFLKDOVVIRTVLNILOTNTSAATSLGTYFLS 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 ISNSLILDVKAEPIDDGKGLNL----SFPVTANVTVAGPIIGQ--IINLKASLDLLTAVT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 IET--DPQTHQP-----VAVLGECASD-PTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 IETFLDKAEDQPHIGKQFVPPMMESVLGDYARNVPDARESEVLSLFATIINKYKATMLDD 821
A.Accession: T52638
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-1075 <-HAA
A.Cross references: EMBL:Y18469; PIDN:CAB89280.1
A.Experimental source: cultivar Columbia; 3wk-old green vegetative Lissue C;Genetics:
                                                                                                                                                               5 KIVILCG----VLTGTSESILDNLGNDLSNVVDKLEP-VLHEGLETVDNTLKGILEKLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.0%; Score 110.5; DB 2; Length 1075;
Best Local Similarity 23.8%; Pred. No. 4.5;
Matches 68; Conservative 46; Mismatches 107; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 VPHIFEAVEQ---CILEMI------TKNFEDYPEHRLKFFSLL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exportin1 (XPO1) protein - Arabidopsis thaliana (fragment) N:Alternate names: protein F2K13_170 C:Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exportin 1 [validated] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T52638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 PQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: xpol
C;Function:
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                  엺
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                         R:Wirels, L.; Ball, W.D.
J. Biol. Chem. 267, 2579-2587, 1992
A:Title: Neonatal rat. submandibular gland protein SMG-A and parotid secretory protein ar
A:Reference number: A42337, MUID:92129360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 267, 2679-2687, 1992
Affilte: Neonattal rat submandibular gland protein SMG-A and parotid secretory protein ar
A:Reference number: A42337; MUID:92129360
A;Accession: A42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ις
·
                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
C:Accession: A42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 DKISISLIGRRIPFVNRILDGVSGLLTGAVSILLQNILCPVLQYLLSTMSGSAIQGHISN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 DCKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GVLQKSSAWQLAKQKAQEAEKLLNNVISKLI,PTN--TDIFG--LKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QLGSLVVLCGLI,IGTSESLLGDVANAVNN------LDILNSPSEAVAONLNLDV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QLWKLVLLCGVLTGTSESLLDNLGN···DLSNVVDKLEPVLHEGLETVD·NTLKGILEKL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: GB:M83210; NID:g206989; PIDN:AAC12783.1; PID:g206990 A:Note: sequence extracted from NCBI backbone (NCBIN:78707, NCBIP:78708) C;Superfamily: parotid secretory protein
180 ISLSLLDKHSQ1:NKFVNSVINTLKSTVSSLLQKEJCPLIR1F1HSLDVNVIQQVVDN 237
                                                      168 ISISELGRREPIINSIEDGVSTELTSTVEONFECPELQYVESTENPSVEQGEESN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M83209; NID:g206456; PIDN:AAC06334.1; PID:g206457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: sequence extracted from NCBI backbone (NCBIN:78709, NCBIP:78710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score 331.5; DB 2; Length 235; 31.7%; Pred. No. 4.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 207.5; DB 2; Length 206; 24.0%; Pred. No. 4.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Mismatches
                                                                                                                                                                                                                     parotid secretory protein precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Gene: Psp
C.Superfamily: parotid secretory protein
C.Keywords: parotid gland; saliva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submandibular gland protein A - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Mirels, L.; Ball, W.D.
J. Biol. Chem. 267, 2679-2687, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 31.7% tes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-235 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-206 <MIR>
                                                                                                                                                                                                                                                   N;Alternate names: PSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B42337
                                                                                                                                                                                                                                                                                                                                           C; Accession: B42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
A)Cross-references: EMBL:X85021; NID:9728698; PIDN:CAA59385.1; PID:9728701
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rikuroda, M.; Ohta, T.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2011.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross-references: GB:BA000018; PJD:913701417; PIDN:BAB42711.1; GSPDB:GN00149
A)Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SA1447 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: :: | | :: | 379 EVELITIDELIYLSEILEDKSQI,VELFEYFISINEDLVLKCL------KSLGLT----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 VTVAGPIIGQIINLKASLDLLTAVTIETD - PQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 -----GELFEIRLTTSLFTNADVNTDIVKQLSDPV----ETTKKDTASFQTFLDKHS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KFVNSVINTLKSTVSSLLQKE1CP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 ELINTTNVSMLTETGERYKKVI,SLFTEAIGKGYKASSFLTSFFTTLESRITFLLRVTISP 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 TKEAIISYLSSDLFKGVGKKTAQNIVNTLG------DNAINDILD----DHSVLEK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 SSAWQLAKQKAQEAEKL-LNNVISKLLPTNTDI-FGLKISNS------------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 VSGLSKKKOK-QIAEQISANQESEKIMIRLHDLGFGPKLSMAIYQFYLGDTLTILDRNPY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 -LILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD----P 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 QLIYDIK-----GIGFNKADQLARNIGIA---YNDNERLKAAL----LYTLEEECIKQG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 SILTFLDKEDKPVCDKFITSYTKSIAKYDRS-----KLNIILSLLKK-----IKLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 EAEKILNNVI--SKILPTNTDI-----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                   48; Mismatches 93; Indels 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          19 SLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 TSESLLDNLGNDL----SNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQK 66
                                                                                                                                                                                                                                                                                             Query Match

8.9%; Score 109; DB 2; Length 1769;
Best Local Similarity 19.2%; Pred. No. 11;
Matches 52; Conservative 48; Mismatches 93; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.8%; Score 108; DB 2; Length 825; Best Local Similarity 24.7%; Pred. No. 4.8; Matches 72; Conservative 39; Mismatches 94; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 AAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                                                    C:Keywords: transmembrane protein
                         A; Residues: 1-1769 <RAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-825 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 OIIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: B89944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B89944
                                                                                                                                                               A; Map position: 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SA1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 5
A:Introns: 33/3; 72/3; 103/3; 127/3; 163/3; 191/2; 237/3; 260/3; 286/3; 307/3; 322/3; 35
08/3; 954/3; 1000/3; 1035/3
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 16-Feb-2001 C;Accession: T51557 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000 A;Reference number: 225394 A;Accession: T51557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, February 1995
A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and A;Reference number: S53376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Rasmussen, S.W.
Yeast 11, 873-883, 1995
A:Title: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drobable membrane protein YUJ109c · yeast (Saccharomyces celevisiae)
N:Alternate names: hypothetical protein J0808
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S53378; S56887; S57359
R;Rasmussen, S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VDLGVLQKSSA-----W-QLAKQKAQEAEKLLNNVISK----LLPTNTD-----IFGLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 ISNSLILDVKAEPIDDGKGLNL----SFPVTANVTVAGPIIGQ--IINLKASLDLLTAVT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 IET--DPQTHQP-----VAVLGECASD-PTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653 RD-EYLQRLMALPNQKWAEIIGQARHSVEFLKDQVVIRTVLNILQTNTSAATSLGTYFLS 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Mismatches 107; Indels 65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KLVLLCG-----VLTGTSESLLDNLGNDLSNVVDKLEP-VLHEGLETVUNTLKGILEKLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1769 <RAW>
A;Cross-references: EMBL:Z49384; NID:g1008292; PID:g1008293; MIPS:YJL109c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.0%; Score 110.5; DB 2; Length 1075;
Best Local Similarity 23.8%; Pred. No. 4.5;
Matches 68; Conservative 46; Mismatches 107; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S57359
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 EKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 VPHIFEAVFQ---CTLEMI-----TKNFEDYPEHRLKFFSLL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-1769 CRAS>
A; Cross-references: EMBL:X85021; NID:9728698; PID:9728701
R; Rasmussen, S.W.
submitted to the Protein Sequence Database, September 1995
A; Reference number: $56876
A; Accession: $56887
                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: cultivar Columbia; BAC clone F2K13 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Note: F2K13_170
C,Superfamily: Arabidopsis thaliana exportin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S57357; MÜID:96090136
                                                                                                                                                                                                                                                                                                        A;Residues: 1-1075 <SAT>
A;Cross-references: EMBL:AL391141
                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S53378
```

Dp

ά g ô qq qq

ô

ò

241 HTYLPINVVIDLTVDVLNYQDEEVIEPEKLDEMLQYLNEEKRLIIDNEQVAIPSLYYSEI 300 216 CPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248	: SAS
301 KSVQNLFRIKTHTNKLTELEQSDLOMHIGELEDANOVNYAASGKEALQTAI 351	
RESULT 8 A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - Staphylococcus carnosus (strain TM300) C.Species: Staphylococcus carnosus C.Species: Staphylococcus C.Species: Staphylococcus carnosus C.Species: Staphylococcus C.Species: Staphylococc	Oy 173 CASDPTSISIS 201 I
eriol. 175, 7495-7499, 1993 Cloning, Sequencing, and characterization of the gene encoding the class I fructince number: A49943; MUID:94042930 Sion: A49943 Preliminary	#ESULT 10 T50073 myosin-like coiled-coil protein sp8 [imported] - fission yeast (Schizosaccharomyces F 7. Species: Schizosaccharomyces pombe
ues: 1-296 - XXII ues: 1-296 - XXIII - references: EMBL:X71729; NID:g297873; PIDN:CAA50663.1; PID:g297874 rds: aldehyde-lyase; carbon-carbon lyase	C.Accession: 150073 R.Accession: 150073 R.McDougall, R.C.: Rajandream, M.A.: Barrell, B.G.; Seeger, K.: Harris, D. submitted to the EMBL Data Library, December 1999 A.Reference number: 225034
Query Match 8 6%; Score 106; DB 2; Length 296; Best Local Similarity 25.9%; Pred. No. 1.7; Matches 50; Conservative 31; Mismatches 64; Indels 48; Gaps 9;	A.Accession: T50073 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-1727 <mcd></mcd>
51 KGILEKLKVDLGVLQKSSAMQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 110	A:Cross_reterences: EMBL:AL133357; PIDN:CAB62414.1; GSPDB:GN00066; SPDB:SPAC1486.04c A:Experimental source: strain 972h(-); cosmid c1486 C:Genetics: A:Genetics: A:Gene: SPDB:SPAC1486.04c
111 VKABPIDDGKGLNLSFPVTANVTVAGPIIGQIIN	A;Map position: 1 Query Match B.5%; Score 104.5; DB 2; Length 1727; Rest local similarity 24.3%; Ored No. 23.
151LLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKF 195 101	
261 SRALVSDLNAQQS 273	49 - TLKGILEKLKVDLGVLQK - SSAWQLAKQ RAOEAEKLLNNVISKLLPTNTDIF 1 1 1 1 1 1 1 1 1
y s Ilgand-binding protein RYA3 - rat S Rattus norvegitaus (Norwey rat) 13-lan-1945 #seemenre revision 13-lan-1945 #foxt chance 05-Nor-1000	Qy 100 GLK1SNSLILDVKABPIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 158 1:
aton: S17448 T.N.; Boehn, T.; Keverne, E.B.; Rabbitts, T.H. 10, 2813-2819, 1991	QY 159 TUPOTHQPVAVLGECASOPTSISILIDKHISQIINKFVNSVINTLKSTVSSLIQKEICPL 218
A;Ittle: Novel genes for potential (igand-binding proteins in subregions of the olfactor A;Reference number: S17447; MUID:92007724 A;Accession: S17448 A;Status: preliminary A;Molecule type: mRNA	Qy 219 IRIF[HSLDVNVIQQVV 235 : : : Db 552 LREKVRALECDVEIGKQTV 570
les: 1-473 <dea> -references: EMBL:X60658; NID:g57733; PIDN:CAA43065.1; PID:g57734</dea>	RESULT 11 G64242
Query Match 8.5%: Score 104.5; DB 2; Length 473; Best Local Similarity 21.0%; Pred. No. 4.1; Matches 60; Conservative 52; Mismatches 93; Indels 81; Gaps 12;	Cytadherence accessory protein (lumw1) homolog MG386 - Mycoplasma genitalium Cyspecies: Mycoplasma genitalium Cybate: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999 CyAccession: G64242
1 LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEK 56	<pre>Kirtaser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann. R. M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C. Science 270, 397-403, 1995</pre>
57'LKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKTSNSLILDVK 112 - - - : -	A;Title: The minimal gene complement of Mycoplasma genitalium. A:Reference number: A64200; MUD:96026346 A;Accession: G64242

g δ g ò ò g

rei

```
A;Note: the four fragments shown in reference A60991 correspond to four types of d with repeats ordered ABCCCDABCUDABCCCDABCCDABCDABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SA2399 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           984 STSVKVQLY---AQLFSTGLNTIYDSIQLVN----LISNAVNDTINVLPTITEGI----- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.5%; Score 104; DB 2; Length 2710;
Best Local Similarity 20.3%; Pred. No. 45;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807 KTLLLDASVSPDTKFILNNLKLNIESSIGDYIYYEKLEPVKNIIHNSIDDLIDEFNLLEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 ITKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 TIETDPQTHQPVAVLGECASDPTSISLELDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: Clostridium difficile toxin A; cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-55,'V',57-2079,'L',2081-2549,'S',2551-2710 <SAU>
A;Cross-references: EMBL:X51797
                                                                                                                                                                                                                                                             Nucleic Acids Res. 18, 1629-1630, 1990
A,Title: Nucleotide sequence of Clostridium difficile toxin A.
A,Reference number: S08637; MUID:90221894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <CP22>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <CP01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <CP06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <CP12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <CP14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CP15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <CP16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CP19>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CP20>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <CP25>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <CP03>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <CP08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <CP09>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <CP10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <CP18>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: cytotoxin; enterotoxin F;1820-1839/Domain: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yeolomor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nomology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                     R; Sauerborn, M.; von Eichel-Streiber,
                                                                                                 A; Cross-references: EMBL: X60984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cpl repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F 2087-2107/Domain: cpl re F 2108-2128/Domain: cpl re F 2108-2128/Domain: cpl re F 2201-2220/Domain: cpl re F 2201-2220/Domain: cpl re F 2201-2241/Domain: cpl re F 2215-2334/Domain: cpl re F 2315-2334/Domain: cpl re F 2315-235/Domain: cpl re F 2315-2397/Domain: cpl re F 2449-2468/Domain: cpl re F 2449-2468/Domain: cpl re F 2469-2510/Domain: cpl re F 2562-2591/Domain: cpl re F 2562-2502/Domain: cpl re F 2562-2502/Domain: cpl re F 2563-2602/Domain: cpl re F 2563-2602/Domain: cpl re F 2653-2602/Domain: cpl re F 2673-2694/Domain: cp
              A; Molecule type: DNA
A; Residues: 1-92 <VON>
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S08638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1840-1860/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1861-1881/Domain:
F;1933-1952/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1953-1973/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1974-1994/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F; 1995-2015/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;2067-2086/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: toxA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C: Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M30307; NID:q144925; PIDN:AAA23283.1; PID:g144926
R;Wren, B.W.; Clayton, C.L.; Tabaqchali, S.
FEMS Microbiol. Lett. 70, 1-6, 1990
A;Title: Vucleotide sequence of Clostridium difficile toxin A gene fragment and detectid A;Reference number: A60991
A;Accession: A60991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin A - Clostridium difficile
C;Species: Clostridium difficile
C;Species: Clostridium difficile
C;Species: Clostridium difficile
C;Species: 3.Jan-1992 #sequence_trains and analyse 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gross references: EMBL:X60984
R;von Elchel-Streiber, C.; Laufenberg-Feldmann, R.; Sartingen, S.; Schulze, J.; Sauerbor
Mol. Gen. Genet. 233, 260-268, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: '1.1894-1899,'K',1901-1910,'Y',1912-1919;2054-2074;2096-2116;2138-2158 <WRE
A; Cross-reference: GB:X17194
R; Eichel-Streiber, C.; Laufenberg-Feldmann, R.; Sartingen, S.; Schulze, J.; Sauerborn, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Title: Comparative sequence analysis of the Clostridium difficile toxins A and B. A.Reference number: S22434; MUID:92293124
A.Accession: S22437
                                                                                                                A;Cross-references: GB:U39723; GB:L43967; NID:g1046092; PID:g1046097; TIGR:MG386 A;Experimental source: strain G-37 C;Genetics: A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, July 1991
A; Description: Comparative analysis of Clostridium difficile toxins A and B. A; Reference number: S21894
A; Accession: S21897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ----LKASLDLL------TAVTIETDPQTHQPVAVL------GECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 ELN----HEEIGNEFIN------716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::::||:|
518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQQEFSEPVVSDEKIKETNSDESVNTDL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 --IFGLKISNSLLLDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQI--IN---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     632 PQEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDLSLELDSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 SKEIKDSAKADLSNISDDIDSVWKEFGSFTDETOKSVEEKSOVDEIILDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 TALFSEKLVNEVLL--TNEYVD----VNAPFSTETEVKVSSELPKSELVDEITFINNDPK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVIQKSSAWQLAKQK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KLLPTNTD----- 97
                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 104; DB 2; Length 1616; 20.6%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AQEAEKLLNNVIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                      A; Residues: 1-1616 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-2710 <DOV>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Residues: 1-154 <EIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 KTQLQT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 TTQLET 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
```

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Contents: annotation C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: XF0816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                     CyAccession: F90067

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, L.; Ogud A.; Khroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Itouwa, H.; Kobayashi, I.; Cul, L.; Ogud T.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUD:21311952; PMID:11418146

A;Reference number: B90067

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 < KUK>
A;Cross-references: GB:BA000018; PID:g13702563; PIDN:BAB43704.1; GSPDB:GN00149
A;Cross-references: strain N315
C;Genetics:
A;Gene: SA2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A) Reference number: 100839
A) Accession: G02157
A) Status: preliminary: Lranslated from GH/EMBL/DDBJ
A) Andecule type: mRNA
A) Residues: 1-1056 <WHI>
A) Cross-references: EMBL:037426; NJD:g1171152; PIDN:AAA86132.1; PID:g1171153
C) Genetics:
A) Genetics: GDB:RNSL1; Eq5; KSP
A) Cross-references: GDB:132856; OMIM:148760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinesin-like spindle protein HKSP - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447 LDQCKSDLQNKTQELE------TTQKHLQETKLQL-VKEEYITSALESTEEKLH 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ----LKASLDLLTA------VTIETDPQTHQPVAVLGECASDPTSISL------ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 EGKYTADYLADKGVVPFLKVDKGLAEEQNGVQLMKP------IDNLDSLLDRANERHI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIIN------ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 FGTKM-RSNILELNEQGIKD--VVEQQFEVAKQIIAKGLVPIIEPEVNINAKDKAEIEKV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: GDB:132856; OMIM:148760
A.Map position: 10q24.1-10q24.1
C.Superfamily: kinesin-related protein Eq5: kinesin motor domain homology C.Keyworts. ATP: nucleotide binding; P-loop F:19.36:/Domain: kinesin motor domain homology < KMOT>
F:19.76:/Domain: kinesin motor domain homology < KMOT>
F:105-112/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQK--SSAWQLAKQKAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 EGLETVDNTL-KGILEKLKVDLGVLOKSSAWOLAKQKAQEAEKLLNNVISKLLPTN-TDI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 100.5; DB 1; Length 1056; 23.0%; Pred. No. 23; tive 39; Mismatches 89; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

8.4%; Score 103.5; DB 2; Length 296;
Best Local Similarity 25.5%; Pred. No. 2.6;
Matches 53; Conservative 30; Mismatches 68; Indels 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 --SLLDKHSQIINKFVNSVINTLKSTVS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 ANELLKDNDELIASFSRALASDLRADQS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 23.09
es 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Accession: G02157
R;Whitchead, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
```

```
Cispecies: Xylella fastidiosa
Cispecies: Xylella fastidiosa
Cispecies: Xylella fastidiosa
Cipacession: 02070 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
Cipacession: 028759
Ranonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Ranonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Ranonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Rature 406, 151-157, 2000
Affilte: The genome Sequence of the plant pathogen Xylella fastidiosa.
Affilte: The genome Sequence of the plant pathogen Xylella fastidiosa.
Affilte: The genome Sequence of Augusta 1990 Asimon Agreed Forman Agraes 1990 Asimon Agra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Franchistors: Ferreira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins chado, M.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Atchero; da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 LDKHSQ--IINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLD------VNVIQQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766 HKQ-----ITDVAAQFKPRIFLIHRPEAQQSLILAGLLAPPTKD------PANLE 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 INVGNEAFGGTFSSRLNMNLREEKHWAYGASSVLPNAQGQRPYVFIAPVQTDKTAESIAE 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         870 IQKEAQDVIVNK-------PLTQEEVDKIKQQIIRSLPGSYETSGAVLDAVES 915
494 DAASKLLNTVEE----TTKDVSGLHSKLDRKKAVDQHNAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                    127 ----PVTANVTVAGPIIGQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                    181 SLSLLDKHSQIINKF----- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 STHV----SQIFNMILKEQSLAAESKTVLQELINVLKTDLLSSLEMILSPTVVSILKINS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 SGTNEAIQSLTATDLKDFQQRWLRPDNVRILVTGHTTLKSIIPQLEAAFGDWQAPSTIKS 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLIL-DVKAEPIDDGKGLNLSFPVTAN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 VTVAGPIIGOIINLKASLDL-----LTAVTIETDPQTHQPVAVLGECASDPTSISLSL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGII.EKLKVDLGVLQKSSAWQL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zinc proteinase XF0816 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 100; DB 2; Length 990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 ---RIFIHSL-----DVNVIQQVVDNPQHKTOLQTL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          653 QLKHIFKTSLTVADKIEDQKKELDGFLSILCNNLHELQENTI 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 VVDNPQHKTQLQTL 247
```

Db 916 IVRYERPDNYIQTL 929

Search completed: August 6, 2002, 17:05:12 Job time: 914 sec

```
Q9np55 homo sapien
P42945 saccharomyc
Q9uK5 schizosacch
Q9uK5 schizosacch
Q9uK5 schizosacch
Q9429 mycoplasma
P1614 clostridium
P52732 homo sapien
P47813 haemophilus
P98676 tomato mosa
P03587 tomato mosa
P03587 tomato mosa
P54861 saccharomyc
C58718 methanococc
Q09459 caenorhabdi
Q05022 saccharomyc
P53076 methanococc
Q09459 caenorhabdi
Q05022 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P18428 homo sapien
P57655 buchnera ap
P33420 saccharomyc
P36097 saccharomyc
P42971 bacillus su
Q9418 tomato mosa
Q10411 schizosacch
Q09624 caenorhabdi
O52705 methanococc
Q92736 homo sapien
P58668 listeria mo
P40668 saccharomyc
                                                                    August 6, 2002, 17:07:31 ; Search time 32.88 Seconds (without alignments) 292.045 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P07743 mus musculu
P97361 mus musculu
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                 1 LOLWKLVLLCGVLTGTSESL.........NVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLUN_HUMAN
YJK9_YEAST
ALF_STACA
ALM1_SCHPO
P200_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOXA_CLODI
EG5_HUMAN
DNLJ_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNM1_YEAST
YGX7_YEAST
RA50_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQ38_CAEEL
RRP5_YEAST
NIFK_METMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LBP_HUMAN
ILVC_BUCAI
                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKPO_TOMK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NI80_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKD3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PBPC_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAP1_HAEIN
                                                   OM protein - protein search, using sw model
                                                                                                                        US-10-020-139-2_COPY_2_249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YD86_SCHPO
                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                  SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
95
94.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99999
92233
92333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359.5
192.5
183.5
109
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
104
100
100
98.5
98.5
98.5
                                                                                                                          Title:
Perfect score:
                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                    Sequence:
                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

P16573 rattus norv O67606 aquifex aeo Q49460 mycoplasma Q00979 schizosacch Q58556 methanococc Q9v7a4 drosophila P12612 saccharomyc Q10339 schizosacch P46939 homo sapien P49022 lactococcus	AA. e) e)	Vertebrata; Euteleostomi; hi; Muridae; Murinae; Mus.	, Harmark K., protein and salivary OTEIN IN THE PAROTID GLAND. TS PRODUCTION IS COORDINATED	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). REMBL: W16806; AAA40009.1; - EMBL: W26806; AAA40009.1; - EMBL: M26806; AAA40009.1; - EMBL	6E2EF3 CRC64; DB 1; Length 235; 7e-20; is 79; Indels 17; Gaps 3;
ECTO_RAT METE_AQUAE V468_MYCGE V468_MYCGE V656_MYCGE V656_MYCGE V656_MYCGE V656_MYCGE V656_MYCGE V656_MYCGE V666_MYCGE V666_	ALIGNMENTS RD; PRT; 235 / Created) Last sequence update Last annotation update tein precursor (PSP)	lata; Craniata; V htia; Sciurognath -2582349; se PSP mRNA.";	A. Mikkeisen B.M. HOWEVER, I	copyright. It is use of Bioinform (S Estitute.) itutions as long in the sea agreement (See agreement (See (Seb Sub.ch)	3 MW; 23311BAE1E6 8, Score 359.5; 88; Pred. No. 4.7 62; Mismatches
7.4 519 7.4 761 7.4 1783 7.3 9025 7.3 1015 7.3 615 7.2 1826 7.2 3433 7.2 3433	STANDA Rel. 08, Rel. 08, Rel. 35,	(Mouse). (Mouse). (Mouse). (Mouse). Mouse. (Mouse).	1-87 FROM N./ TISSUE=Spleer 4556; pubmed- 4566; pubmed- 4566; pubmed- 4506; pubmed- Hjorth J.P nof murine posion. 19511896(1986 1: psp IS THE	Swiss Institution is Swiss Institution in the Swiss Institution in this statem with the Swiss and Incomplete and Incomplete in the Swiss Institution in the Swiss Instituti	E 235 AA; 24753 th 29.38 Similarity 33.68 80; Conservative
334 335 337 337 337 337 337 337 337 337 337	MOUSE PSP_MOUSE PO7743; 01-AUG-1988 01-AUG-1988 01-NOV-1997 PATOLIG SECT PSP.	Mus musculus (Mouse). Eukaryota; Metazoa; C. Mammalia; Eutheria; R. NCBL_TAXID=10090; [1] SEQUENCE FROM N.A. TISSUE-Parotid gland; MEDLINE-85215456; Pub Madsen H.O., Hjorth J Madsen H.O., Hjorth J Molecular cloning of	L1 L2 L2 L2 L3 L3 L3 L3 L3	CC This SWISS-PR CC between the CC use by non- CC modified and CC entities requ CC erities requ CC remely x0680; DR EMBL; M2680; DR EMBL; M268	Query Match Best Local Simi
	RESU PSP- 1D DT DT DT GN	R R R R R C C C C C C C C C C C C C C C	2000 X 4 X X X X X X X X X X X X X X X X	00000000000000000000000000000000000000	SQ Qu Bee Ma

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weston W.M., Leclair E.E., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan K.S., Greene R.M.;
"Differential display identification of plunc, a novel gene expressed in embryonic palate, nasal epithelium, and adult lung.":
J. Biol. Chem. 274:13698-13703(1999).
                                                                             62 GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSLILDVKAEPIDDG 119
                                                                                                                                                        120 KGLNLSFPVTANVTVAGPLIGQ1INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS 179
                                                                                                                 51 ELLOQATSWPLAKNSILET---LNTADLGNLKSFTSLNGLLKINNLKVLDFOAKLSSNG 107
                                                                                                                                                                                              108 NGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGKCSSNTDK 167
                                     3 QLGSLVVLCGLLIGNSESLLGELGSAVNN------LKILNPPSEAVPQNLNLDV 50
2 QLWKLVLLCGVLTGTSESLLDNLCNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                  180 ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic organization of the mouse plunc gene and expression in the
                                                                                                                                                                                                                                                           progression (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- TISSUE SPECIFICITY: Upper airways, nasopharyngeal regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeClair E.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weston W.M., Leclair E.E., Trzyna W., McHuyh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys. Res. Commun. 284:792-797(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
J. Biol. Chem. 275:8262-8262(2000).
                                                                                                                                                                                                                                                                                                                                                                              278 AA
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21290678; PubMed=11396972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99240770; PubMed=10224143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMŖL; AF356785; AAK63069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developing airways and thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U69172; AAB63256.1; -. MGI:1338036; Plunc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Palate;
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thymus
                                                                                                                                                                                                                                                                                                                                                                                  PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                       P97361;
                                                                                                                                                                                                                                                                                                                                                             PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                õ
                                                                                                                             g
                                                                                                                                                                     ò
              õ
                                                  g
                                                                                          ò
```

Signal; Repeat.

```
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLUM. HUMAN STANDARD: FRI, 22. ...
09NP55; 09NZT0:
16-CGT-2010 (Rel. 40, Created)
16-CGT-2010 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
protein) (Lung specific X protein) (Masopharyngeal carcinoma-related
protein) (Tracheal epithelium enriched protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 INEKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 LQLAVKLNITAEVLAVKDNOGRIH---LVLGDCTHSPGSLKISLLNGVTP-VQSFVDNLT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                  86 NVISKL---LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GLLGKLTSSVPLLNNILDIKITDPQLLELGLVQSPDGHRLYVTIPLGLTLNVNMPVVGSL 174
                                                                                                                                                                                                                                                                                                                                                                                             67 NPTDLLAGKFTDALSGGL-----LSGGL-----LGILENIPLLDVIKSGGGNSNGLVG 114
                                                                                                                                                                                                                                                                                                                        7 LVVLCGLLAHSTAQLAGLPLPLGQGPPLPLNQGPPLPLNGGQLLPLAQGLPLAVSPALPS 66
                                                                                                                                                                                                                                                                                                                                                             30 NVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iwao K., Watanabe T., Fujiwara Y., Takami K., Kodama K.,
Higashiyama M., Yokuuchi H., Ozaki K., Monden M., Tanigami A.;
"Isolation of a novel human lung-specific gene, LUNX, a potential
molecular marker for detection of micrometastasis in non-small-cell
                                                                                                                                                                                                                                                      61; Gaps
                                                                                                                                                                                                                                                                                       6 LVLLCGVLTGTSESLLD-----S 29
POTENTIAL.
PROTEIN PLUNC.
4 X 6 AA REPEATS OF G.[LPQ]-[PL]-L-P-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bingle C.D., Bingle L., "Characterization of the human plunc gene, a gene product with an upper airways and nasopharyngeal restricted expression pattern."; Biochim. Biophys. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Melazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
7F40BED9859188FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Z.W., Yao K.T., Xu L.G., Ren C.P., Lan K., Xie L., Zhang L.
Liu W.D., Zhou W., Wang L.;
                                                                                                                                                                                                                    DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 NTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 GILTKVLPELIQGKVCPLVNGILSGLDVTLVHNIAELLIHGLQ 273
                                                                                                                                                                                                                                                          48; Mismatches 107;
                                                                                                                                                                                                                                       Pred. No. 1.6e-07;
                                                                                                                                                                                                                      15.7%; Score 192.5;
                                                                         REPEAT 2.
REPEAT 3.
REPEAT 4.
                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21150203; PubMed-11251963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20472055; PubMed=11018263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer 91:433-437(2001).
                                                                                                                                                                     28611 MW;
                                                                                                                                                                                                                                         23.78;
                                                                                                                                                                                                                                                            67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCB1_Tax1D-9606;
                                                                                                                                                                                                                           Query Match
                                                                                                                                   CARBOHYD
                                                                                                                                                                     SEQUENCE
                                                                                                                                                    CARBOHYD
                                                           REPEAT
REPEAT
                                            DOMAIN
                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLUN_HUMAN
                                                                                                                 REPEAT
                         CHAIN
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                   ò
         FT FT FT FT SO S S O S
```

```
this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                               RN 14J

Beloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Almedda J.P., Babbaye A.K., Bagguley C.L.,

RA Bailey J., Ballow K.F., Bates K.N., Beard L.M., Brown A.J.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,

RA Coulson A., Coville G.J., Deadman R., Dhaml P., Dunn M.,

RA Coulson A., Coville G.J., Deadman R., Dhaml P., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A. French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A. French L., Garner P.,

RA Fington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Lavid G.K., Lawlor S.,

RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RAY M.P., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay S.,

RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Swan M., Sycamore M.J.F., Scotter U.B., Shownkeen R., Sims S.,

RA Swan M., Sycamore M., Sycamore N., Taylor R., Walliams S.A.,

RA Swan M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Swan M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Mitchead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Mining L., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Bertley D.R.,

RA Mining L., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Williams S.A.,

RA Mitchead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA Mitchead S.L., Whittaker P., Willey D.L., Williams S.A.,

RA Williams S. Williams S.A.C., Vardon M. W. Walliams S.A.,

RA Williams S. Williams S.A.C., Vardon M. W. Walliams S.A.,

RA Williams S.L., Whittak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lindahl M., Stahlbom B., Tagesson C.:
Lectrophoresis 22:1795-1800(2001).

Lectrophoresis 22:1795-1800(2001).

Lectrophoresis 22:1795-1800(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: Upper airways and nasopharyngeal regions, including trachea and masal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The DNA sequence and comparative analysis of human chromosome 20.\ "; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PROTEIN PLUNC.
9 - X (IN REF. 1; AAF70860).
EDF152FBC35315BC CRC64;
"Cloning a new gene related to nasopharyngeal carcinoma."; submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 95-152; 157-167 AND 214-232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and some other types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBČELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21317946; PubMed=11425234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL121901; CAC03549.1; -. EMBL; BC012549; AAH12549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF214562; AAG13653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB024937; BAA93633.1; -. AF158745; AAF82622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 220 C
256 AA; 26712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF172993; AAF70860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way undified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 SILTFLDKEDKPVCDKFITSYTRSIARYDRS-----KLNIILSLLKK-----IRLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A 37.5 Kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar to the DALBO gene, and a tRNA(Arg)."; xeast 11:873-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SLIDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 78
                                                                                                                                               74 KQKAQEAEKLLNNVISK----LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                       131 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                       138 KLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHL-VLGDCTHSPGSLQISLLDGLG 196
                                                                                                                                                                                78 KPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSPDGHRLYVTIPLGI 137
                                                                       14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                          Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                              190 QI-INKEVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14-Ppothetical 200.0 kDa protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 109; DB 1; Length 1769;
14.9%; Score 183.5; DB 1; Length 256; 23.8%; Pred. No. 6.9e-07; tive 46; Mismatches 100; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1769 AA; 200080 MW; 064480D1D249B241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
-:- SIMILARITY: CONTAINS 1 HEAT REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288C / FY1679;
MEDLINE=96090136; PubMed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000357; HEAT_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249384; CAA89404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X85021; CAA59385.1;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S0003645; YJL109C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
REPEAT 1729 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 52; Conserva
                              Best Local Similarity
Matches 56, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YJI109C OR J0808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                      YJK9_YEAST
P42945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                  δλ
                                                                                                                                                                                                       a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       132 VTVAGPIIGQIINLKASLDLLTAVTIETD--PQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                               426 ------GELFEIRLITSLFINADVNTDIVKQLSDPV----FTTKKDTASFQTFLDKHS 473
                                                                                                                                                                                                                                                 -----KFVNSVINTLKSTVSSLLQKEICP 217
                                                                                                                                                                                                                                                                                                      474 ELINTINVSMLTETGERYKKVLSLFTEAIGKGYKASSFLTSFFTTLESRITFLLRVTISP 533
                                                        379 EVRLIITDLIYI.SELLEDKSQLVELFEYFISINEDLVLKCL-----KSLGLT----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
79 EAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marke ..., usera, 175:7495-7499(1993).

-i Bacteriol. 175:7495-7499 (1993).

-i CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate - glycerone phosphate + D-glyceraldelyde 3-phosphate.

-i- PATHWAY: SIXYHI STEP IN GLYCOLYSIS.

-i- SIMPLARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOYPHATE ALDOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHIFF-BASE WITH DIHYDROXYACETONE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
A189E75574F1FCC0 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacteria: Firmicutes; Bacillus/Staphylococcus.
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; PF00274; glycolytic_enzy; 1.
Probom; PD001128; Aldolase_1; 1.
PROSITE; PS00158; ALDOLASE_CLASS_1; FALSE_NEG.
Lyass; Schiff base; Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AA.
                                                                                                                                                                                                                                                                                                                                                                                     218 LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                             534 AAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 175:7495-7499(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94042930; PubMed=8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR000741; Aldolase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94042930; Pubmed=8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AA; 32720 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kula M.R., Brockamp H.P.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus carnosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S33358; S33358.
PIR; A49943; A49943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P14223; 1A5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Goetz F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Witke C., Goetz F.
J. Bacteriol. 175:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  ........NIIO 061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyase; Sc
INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALF_STACA
007159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALF_STACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SO THE TWO DAYS A RESTRICT TO THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                               ŏ
                                                                                                                                                              ⋩
                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                     \stackrel{>}{\sim}
                                          ∑
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                 ..
ص
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jimenez M., Petit T., Gancedo C., Goday C.;
"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          151 -----LTAVTIET------DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKF 195
                                                                                                                                                                                                                                          203 KKDQYVMLKLTIPTKVNAYSELJEHPQVIRVVALSGGYSRDEAN---KILKQNDGLIASF 259
                                                                                                                                       111 VKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIIN---------LKASLD-- 150
                                                                                                                                                                        145 NNKEAIE--KVVKQQFEVAKEJIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 202
                                                                 51 KGILEKLKVDLGVLQKSSAMQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 110
                                                                                                     93 KGIVPFLKVDKGLAEEADGVQLMK-PIPDLDKLLDRA-----NERGIFGTKM-RSNILE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,
CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and analysis of GFP-gene fusion library of fission
Match 8.6%; Score 106; DB 1; Length 295; Local Similarity 25.9%; Pred. No. 0.5; es 50; Conservative 31; Mismatches 64; Indels 4es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Fungi; Ascomycota: Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abnormal long morphology protein 1 (Sp8) ALM1 OR SPAC1486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL133357; CAB62414.1; --
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                               196 VNSVINTLKSTVS 208
                                                                                                                                                                                                                                                                                                                              260 SRALVSDLNAQQS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOKINESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-968 H90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ding D.;
                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        ALM1_SCHPO
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                   100 GLKISNSLILDVKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 158
                                                                                                                                                                                                                                                                                                                                                                                                                  449 -LETSNNNLTKVQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSR 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 NVPATVQ--VALDEYAQNPSTASETLVNK--ELAN-----FSSIKEAVSKTLE---- 551
                                                                                                                                                                                                                                                                              333 SENSIRELQEKYDSVVSELQVVKENKNTSVSAGVGLFSPLAQKLSAVQNPEFSFTKVYSD 392
                                                                                                                                                                                                                                                                                                                                                 393 NMKLQQKVSSLKLQLDRLTNKFSSFCEQVKQRIPVVKQQRSEIVRNNIYMNFLSES---- 448
                                                                                                                                                                                                                61; Gaps
                                                                                                                                                                                                                                               17 SESLLDNLGNDLSNVVDKLEPV------48
                                                                                                                                                                                                                                                                                                                49 --TLKGILEKLKVDLGVLQK--SSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIF 99
                                                                                                                                                                               DB 1; Length 1727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. Bacteriol. 175:7918-7930(1993).
-!- FUNCTION: COULD BE A ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE (BY SIMILARITY).
                                                                                                                                                                                            pred. No. 6.3;
41; Mismatches 94; Indels
                                                                                                                                F820BF8D9C132644 CRC64;
         COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPC00_MYCGE STANDARD;
049419; 049259; 049298; 049352; 049353;
01-NOV-1997 (Rel. 35, CreaLed)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                               8.5%; Score 104.5; C
24.3%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; Pubmed=8253680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AICC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                              443 463 COILE
542 740 COILE
804 1106 COILE
1223 1427 COILE
1497 1555 COILE
1601 1664 COILE
1727 AA: 197858 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 IRIFIHSL--DVNVIQOVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 LREKVRALECDVEIGKQTV 570
                                                                                                                                                                                                                    63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma genitalium.
              361
463
740
1106
11555
1664
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein P200.
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing.
                                                                                                                                      SECUENCE
                  DOMAIN
                                  DOMAIN
                                                DOMAIN
                                                                 DOMAIN
                                                                                   DOMAIN
                                                                                                   DOMAIN
                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P200_MYCGE
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                         οy
 KW
FT
FT
FT
FT
FT
SQ
SQ
```

```
14;
          the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a License agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 SLFRDEVVNNIDSQINETVSEQQFEPTYSVNEFQQEFSEPVVSDEKIKETNSDESVNTDL 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 --IFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQI--IN---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ----LKASLDLL------TAVTIETDPQTHQPVAVL------GECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 POEGLEYKVOFLETEPKSLFDEKTTIVVESEPPFIOPDLSLELDSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 SKEIKDSAKADLSNISDDIDSVWKEFGSFTOETQKSVEEKSQVDEILLDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                                                                              17 SESLIDNIGNDISNVVDKLEPVLHEGLETVDNTLKGTLEKLKVDLGVLQKSSAWQLAKQK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- KLLPTNTD---- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                48; Mismatches 75; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1616;
                                                                                                                                                                                           Structural protein; Repeat; Complete proteome. 1389 2 X 32 AA REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VPI 10463;
MEDLINE=90221884; PubMed=2109310;
MEDLINE=90221884; Von Eichel-Streiber C.;
"Nucleotide sequence of Clostridium difficile toxin A.";
                                                                                                                                                                                                                                                                                              P -> S (IN REF. 2).
S -> F (IN REF. 2).
Mw; 6AF76A13AC49E4FF CRC64;
                                                                                                                                                                                                                                      1-2.
2 x 26 AA REPEAT.
2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 104; DB 20.6%; Pred. No. 6.3;
                                                                                                                                EMBL, U02245; AAA03401.1; ALT_FRAME.
EMBL: U02175; AAD12458.1;
EMBL: U02126; AAD12402.1;
                                                                                                                                                                                                                                                                                                                             1616 AA; 185678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 AQEAEKLLNNVIS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: | :| |:|:|
| 692 ELN----HEEIGNEFIN-----
                                                                                                       EMBL; U39720; AAC71613.1; -. EMBL; U02245; AAA03400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 20.69
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                           1236
                                                                                                                                                                                                                                                                   1186
1339
256
304
                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KTQLQT 246
                                                                                                                                                                                                             1205
1205
1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 TTQLET 722
                                                                                                                                                                                                                                                     891
1161
1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOXA OR TCDA.
                                                                                                                                                                                                Cytadherence;
                                                                                                                                                                                MG386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOXA_CLODI
P16154;
                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roxin A.
                                                                                                                                                                                                                                                       DOMAIN
REPEAT
                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
TOXA_CLODI
                                                                                                                                                                                   TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
Kinesin-related motor protein Eq5 (Kinesin-like spindle protein HKSP) (Thyroid receptor interacting protein 5) (TRIP5) (Kinesin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPINDLE. BLOCKING OF EGS PREVENTS CENTROSOME MIGRATION AND ARREST CELLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS. SUBUNIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 819-868 FROM N.A. MEDLINE-95295737; PubMed=776974; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: PHOSPHORYLATED EXCLUSIVELY ON SERINE DURING S PHASE, BUT ON BOTH SERINE AND THR-927 DURING MITOSIS, SO CONTROLLING THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING
                                                                                                                                                                                                                                                  Blangy A., Lane H.A., D'Herin P., Harper M., Kress M., Nigg E.A.; "phosphorylation by p34cdc2 regulates spindle association of human Eg5, a kinesin-related motor essential for bipolar spindle formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T->A: NO MITOTIC PHOSPHORYLATION. NO BINDING TO SPINDLE APPARATUS.
                                                                                                                                                                                                    SEQUENCE FROM N.A., PHOSPHOKYLATION SITE THR-927, AND MUTAGENESIS. MEDLINE-96128120; PubMed-8548803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                               Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead C.M., Rattner J.B.; "Expanding the role of HSEGS within the mitotic and post-mitotic "Expanding the role of HSEGS within the mitotic and post-mitotic phases of the cell cycle."; ". | 111:2551-2561(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Microtubules; ATP-binding; Coiled coil; Mitosis;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11. Endocrinol. 9:243-254(1995).
- FUNCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIPOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E322F2141BEF1601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY CDC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNS -> EL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98369052; PubMed-9701554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRESENCE OF THYROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ro; IPR001752; kinesin.
PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X85137; CAA59449.1; -. EMBL; U37426; AAA86132.1; -. EMBL; L40372; AAC41739.1; -.
                                                                                                                                                                                                                                                                                                                                                     Cell 83:1159-1169(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
480
764
1112
927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     674 67
1057 AA;
                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLY PROPHASE)
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_Tax!D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY
                                                                               KNSI, OR EGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 148760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             984 STSVKVQLY---AQLESTGLNTIYDSIQLVN----LISNAVNDTINVLPTITEGI---- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG----- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      927 ITKEISTIKNSIITDVNCNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     807 KTLLLDASVSPINTKFILNNLKLNIESSIGDYIYYEKLEPVKNIIHNSTDOLIDEFNILEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
--- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833 AA REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF FIVE
                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN ENTERAL ENTEROTOXIN CALLED A AND CYTOTOXIN B. ONLY AFTER THE ENTERAL DELIVERY OF THE ENTEROTOXIN A MAY THE CHARACTERISTIC DISEASE
                                                                                                                                                                       "Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.5%; Score 104; DB 1; Length 2710; 20.3%; Pred. No. 12;
                                                                                                                    Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALLED PSEUDOMEMBRANOUS COLITIS BE INDUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EG5_HUMAN STANDARD: PRT; 1057 AA. P52732; Q15716; 01-577-1996 (Rel. 34, Created) 01-677-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                        Nucleic Acids Res. 18:1629-1630(1990).
                                                                                                               MEDLINE-90129305; PubMed-2105276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01473; CW_binding_1; 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002479; CW_binding.
                                                                                                                                                                                                                            Infect. Immun. 58:480-488(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X51797; CAA36094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAA63564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             DIFFERENT OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M30307; AAA23283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 20.3
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       REPETITIVE STRUCTURE.
                                                                                                                                                                                                                                                                                                  STRAIN=VPI 10463;
von Eichel-Streiber C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; Enterotoxin.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                              STRAIN=VPI 10463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X92982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $08638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
EG5_HUMAN
ID EG5_HI
AC P5273;
DT 01-OC1
DT 01-OC1
DT 01-OC1
```

SOW KRANG PROCESS OF THE PROCESS OF

qq

δλ

Dp ٥y qq δ

δ

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome
                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRPO_TOMK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTIGERACE 769:496-512(1995).
SCIENCE 269:496-512(1995).
-!- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER
-!- FUNCTION: THIS PROTEIN AND 3' HYDROXYL GROUPS IN DOUBLE-
LINKAGES BETWEEN 5'- PHOSPHORYL AND 3' HYDROXYL GROUPS IN DOUBLE-
STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR
STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR
THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNCE FROM N.A. ATCC 51907;

STRAIN-ED / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Relaschmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goodyn J.D., Shiriey R., Liu L.I., Glodek A., Kelley J.M., Schiffer B. Phillips C.A., Spriggs T., Baudek D.M., Brandou R.C., Winyen D.T., Saudek D.M., Brandou R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                             494 DAASKILNIVEE----TTKDVSGLHSKLDRKKAVDQHNAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                             127 -----PVTANVTVAGPIJGQIINEKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                           550 KDGSSKQKAMLEVHKTLFGNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                                                                                                                                          181 SLSLLDKHSQ11NKF-------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 227
                                                                                                                                                               79 E-AEKLLNNVISKLLPTNTDIFGL.-KISNSLILDVKAEPIDD--GKGLNLSF----- 126
                                                                                                                               447 LDQCKSDLQNKTQELE-----TTQKHLQETKLQL-VKEEV1TSALESTEEKLH 493
                                                                       Gaps
                                                                                                21 LDNLGNDLSNVYDKLEPVLHEGLETVDNTLKGIJEKLKVDLGVLQK--SSAWGLAKQKAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase (NAD+1).
LIGN OR LIG OR HI1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- CATALYTIC ACTIVITY: NDD(+) + {deoxyribonucleotide}(N) + {deoxyribonucleotide}(M) = AMP + nicotinamide nucleotide + {deoxyribonucleotide}(M+M). {deoxyribonucleotide}(N+M). -:- SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY. -: SIMILARITY: CONTAINS I BRCT DOMAIN.
                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Protecbacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus
                                       8.1%; Score 100; DB 1; Length 1057; 24.4%; Pred. No. 7.2;
                                                                         79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679 AA.
                                                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE REACTION. IT IS ESSENTIAL DAMAGED DNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
                                                                24.48;
                                                                Best Local Similarity 24.4%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus
                                                                                                                                                                                                                                                                                                                                                                        228 VN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNLJ_HAEIN
P43813;
                                                                                                                                                                                                                                                                                                                                                                                                        650 IN 651
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNLJ_HAEIN
```

ò qq

QΩ

9. 0.5 δ

qq

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P89676: P90349;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-Methyltransicarse/RNA helicase (R. 47/HEL) (126 kDa protein)
17-0mato mosaic virus (strain Kazakh K2) (TOMY) (TMY strain K2)
17-0mato mosaic virus (strain Kazakh K2) (TOMY) (TMY strain K2)
17-0mato mosaic virus (strain double viruses) (TOMY) (TMY strain K2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biol. (Mosk) 31:826-830(1997).
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 VVIRRAGDVIPOII-----GVLHERRPDNAKPIIF------PINCPVC----DS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 TLLNDVEFQVGRTGAITPVAKLEP--VFVAGVTVSNATLHNG-----DEIERLNIAIGDT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ANVIVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 KLLNNV------1SKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 NLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLGKSSAWQLA-KQKAQEAE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K.; "Properties and structure of the tobacco mosaic virus strain K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 QIINKFVNSVINTLKSTVSSLLQKEICPLIRIFI--HSLDVN-----VIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 QITRIEGEAVARCTGGLFCAAQRKE---ALKHFVSRKAMDIDGVGGKLIEQLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligase; DNA repair; DNA replication; NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 99; DB 1; Length 679; 23.1%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                DNA_ligase_N.
DNA_ligase_OB.
DNA_ligase_2BD.
                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00292; BRCT; 1.
SMART; SM00278; HhH1: 2.
SWART; SM00532; LIGANC; 1.
PROSITE; PS50172; HRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
PROSITE; PS01056; DNA_LIGASE_N2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98012318; Pubmed-9454068;
                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD003944; DNA_ligase_N: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRCT.
                                                                                                                                                                                                                                                                 Piam; PF00533; BRCT; 1.
Pfam; PF01553; DNA_ligase_N; 1.
Pfam; PF03120; DNA_ligase_OB; 1.
Pfam; PF03119; DNA_ligase_ZBD: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 23.1%;
                                                EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                                                             HHH_].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                    InterPro; IPR001357; BKCT.
InterPro; IPR001679; DNA_1
                                                                                                                                                                                                                      HHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 1
679 AA;
                                                                                                                                                                                                                                           InterPro; 1PR003583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB1_TaxID=138312;
                                                                                                                                                                         InterPro; IPR004150;
                                                                                                                                                                                                InterPro; IPR004149;
                                                                                                                                                                                                                      InterPro; IPR000445;
                                                                                1B04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - i - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00633;
                                                                                   087703;
                                                                                                     TIGR; H11100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRPO_TOMK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA (CAPPING AND AN RNA HELICASE.
-:- MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CUDON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PORSON 7041352;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7, 48) (183 kDa protein) (Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein);
Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein);
Tomato mosaic virus (strain L) (TOMY) (TMY strain tomato).
Viruses; SSRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome and comparison with the common strain genome.";
J Biochem. 96:1915-1923(1984).
-i- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640 EEP-SIRGSMAKGELQLAGLSGDVPESSYTRSEEIESLEOFHWATASSLJIKQMGSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSKDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the tobacco mosaic virus (tomato strain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohno T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
-i- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON HAG OCCURS
BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                           pfam; PF00978; RNA_dep_RNApol2; 1.
pfam; PF01443; Viral_helicasel; 1.
pfam; PF01460; Vmethyltransf; 1.
Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-DIRECTED RNA POLYMERASE.
METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2F5CE0C8C965336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.0%; Score 98.5; I
20.4%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                  Interpro; IPR001788; KNA_dep_RNApol2.
Interpro; IPR002588; V_methyltransf.
Interpro; IPR00606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85157522; PubMed=6549393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1616 AA; 183614 MW;
                                                                                                                                                                                                                                                           EMBL; Z92909; CABU7439.1; T. EMBL; Z92909; CABU7438.1; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 FIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=12252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRPO_TOML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRPO_TOML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  > ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ☆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oyykol (1973)

Oyykol (1973)

16-007-2001 (Hel. 40, Last sequence update)

16-007-2001 (Rel. 40, Last sequence update)

16-007-2001 (Rel. 40, Last sequence update)

16-007-2001 (Rel. 40, Last sequence (EC 2.7.7.48) (183 kDa protein) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein)]

Nethyltransferase/RNA helicase (MY/HEL) (126 kDa protein)]

Tomato mosaic virus (strain 5-1) (ToWV).

Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHMATASSLIHKQMCS1--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 JDDGK------GLNLSF--PVTANVTVAGPIJGQIJNLKASLDLLTAVTIETDPQT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA-----LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 KLKVDLGVLQXSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou X., Xue C., Chen Q., Qi Y., Li D.; "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                               Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                                                    METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
W; A8EC8929B5CF7CAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKT; 1616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 98.5; L
20.4%; Pred. No. 16;
                                                                                                                                                                                                            InterPro; IPR001788; RNA_dep_RNApol2.
                                                                                                                                                                                                                            Interpro; IPR002588; V_methyltransf.
Interpro; IPR000606; Viral_helicasel.
Pram; PF00978; RNA_dep_RNApol2; 1.
Pram; PP01443; Viral_helicasel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                183564 MW;
                                                                                                                                                                                                                                                                                                         Piam; PF01660; Vmethyltransf;
                                                                                                                                                          EMBL; X02144; CAA26085.1; -. EMBL; X02144; CAA26082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 FIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                    833 84
1616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=138314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                     PIR; A04195; WMTM8T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        ONIB_GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.":
Yeast 12:693-708(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 KLKVDLGVLQKSSAMQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKTSNSLILDVKAEP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 IDDGK-------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 MTAAKVIVAVMSNESGLTLLTFEQPTEANVALA~~~~LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHMATASSLIHKOMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammie A.E., Kurihara L.J., Vallee R.B., Rose M.D.;
"DNML, a dynamin-related gene, participates in endosomal trafficking
in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina: Saccharomycetes;
                                                                                                                                                                                                                                                                         Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1 116 METHYLIRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 98.5; DB 1; Length 1616; 20.4%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).

W; 5DBBFB2FADCC5C0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dynamin-related protein DNM1 (EC 3:6.1.50)
DNM1 OR YLL001W OR L1381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                       Interpro; IPR001788; RNA_dep_RNApol2.
Interpro; IPR002588; V_methyltransf.
Interpro; IPR00606; Viral_helicasel.
                                                                                                                                                                                                                Pfam; PF00978; KNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / FY23;
MEDLINE-96405918; PubMed-8810043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95348179; PubMed-7622557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Biol, 130:553-566(1995).
                                                                                                                                                                                                                                                                                                                                                     183542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
                                                                                                                 EMBL; AJ132845; CAB36997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miosga T., Zimmermann F.K.;
                                                                                                                                      EMBL; AJ132845; CAB36998.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 FIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                    840
                                                                                                                                                                                                                                                                                                                                    833 84
1616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNM1_YEAST
P54861;
                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNM1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 -----OTEQELARYGGVGATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 SESLKLAREVDPQGKRTIGVITKLD-LMDSGTNALD-ILSGKMYPLKLGFVGVVNRS--- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QLAKQKAQEAEKLLNNVISKLLPTNTDIF------GLKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 ---QQDIQ-----LNKTVEESLDKEEDYFRKHPVYRTISTKCGTRYLAKLL----- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 SESL-----LDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD-LGVLQKSSAW 70
                                                          Vandenbol M., Portetelle D., Hilger F.;
Vandenbol M., Portetelle D., Hilger F.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MICKOTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN THAT
PARTICIPATES IN EMDCYTOSIS. DOES NOT APPEAR TO PARTICIPATE IN
SECRETION OR VACUOLAR PROTEIN SORTING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-6cT-1996 (Rel. 34, Created)
01-6cT-1996 (Rel. 34, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-6ST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 97; DB 1; Length 757; 23.1%; Pred. No. 7.8; tive 35; Mismatches 74; Indels
                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: GTP + H(2)0 = GDP + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H -> ISPD (IN REF. 1);
; EBEF8793C5951770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 TSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 NESRASLV---LOLMNKFSTNFISSIDGTSSDINTKELCGGARIY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; Smooth Company of the Martin Smooth Company of the Motor protein; GTP binding. Hydrolase; Motor protein; GTP binding. A 2 GTP (POTENTIAL). The Motor protein; GTP (POTENTIAL). The Motor protein of the Motor Company of the Motor Compan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000375; Dynamin_central.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 247 G
244 247 G
124 124 H
757 AA; 84971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0003924; DNM1.
InterPro; IPR001401; Dynamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01031; dynamin_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L40588; AAA99998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X91488; CAA62769.1; -. Z73106; CAA97444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00350; dynamin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity 23.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00195; DYNAMIN. SMART; SM00053; DYNC; 1. SMART; SM00302; GED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003130; GED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02212; GED;
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGX7_YEAST
P53076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGX7_YEAST
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
N CBI_TaxID-4932;

N CBI_TaxID-4932;

N CBI_TaxID-4932;

P SEQUENCE FROM N.A.

Rartmann B., Kramer W.;

L Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

C This SWISS-PROT entry is copyright. It is produced through a collaboration to between the Swiss Institute of Bioinformatics and the EMBL outstation.

C between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way c medities requires a license agreement (See http://www.isb-sib.ch/announce/corsend and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/corsend and email to licensewisb-sib.ch).

R EMBL: 272749; CAA96943.1; CAA
```

Search completed: August 6, 2002, 17:07:32 ob time: 874 sec

```
P79124 bos taurus
P79125 bos taurus
Q94734 mus musculu
Q6471 rattus norv
Q63550 rattus norv
Q96bK6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            094794 mus musculu 09443 mus musculu 0946p0 mus musculu 0949j6 mus musculu 0949j6 momo sapien 095mv6 arabidopsis
                                                                               August 6, 2002, 17:09:28; Search time 111.35 Seconds (without alignments) 385.296 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q61114 mus musculu
Q9d6p2 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96dr5 homo sapien
Q96dr5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               1 LOLWKLVILCGVIJTGTSESL.....NVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                             562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                   US-10-020-139-2_COPY_2_249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BQP8
Q9SMV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q63471
Q63550
Q96HK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BQQ0
Q96DR5
P79124
P79125
Q9D734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q61114
Q9D6P2
Q9D794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09CQX3
09D6P0
09D9J8
                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_19:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                               sp_fundj:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
129
110.5
                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148.5
148.5
148.5
145.5
                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331.5
207.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150.5
                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                  Sequence:
                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

8.8 825 16 099TNO Q99TNO cubbylococ 8.4 473 11 065701 rattus ratt 8.4 296 16 099R31 099731 stathylococ 8.1 50 16 09PF62 099738 streptococcus 8.1 50 16 09PF62 094178 095436 095442 095442 095442 095442 095442 095442 095444 095444 05544 095444 056454 095444 056454 095444 05644 05644 056454 05644 05644 05644 05644 05644 05644 05644	ALIGNMENTS	PRELIMINARY; PRT; 249 AA. 0, N-2001 (TrEMBLrel: 17, Created) N-2001 (TrEMBLrel: 17, Last sequence update) N-2001 (TrEMBLrel: 17, Last sequence update) 10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.2 sepiens (Human). 10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.3 sepiens (Human). 10.4 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.4 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30). 10.5 sepiens (Human). 10.6 sepiens (SIMILAR TO BSP30). 10.6 sepiens (SIMILAR TO BSP30). 10.7 sepiens (SIMILAR TO BSP30). 10.8 sepiens (SIMILAR TO BSP30). 10.9 sepiens (SIMILAR TO BSP30). 10.0 sepiens (SIMILAR TO BSP30). 10.1 sepiens (SIMILAR TO BSP30). 10.0 sepiens (SI	2 1 1 1 2
7		98600 1-CUGO 1-C	
		RESULT 098000 ID 099000 DT 099000 DT 01900 DT 01	

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                       241 KTQLQT 246
                                                                                                                                                                                                                                                                                                                                                                                 234 TTOQES 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                P79125
                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BSP30.
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                        Q
Q
                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                       ŏ
  RL SO S
                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haigh B.J., Wilkins R.J., Wheeler T.T.; "The cloning and sequencing of two cDNAs coding for alternate forms of
                                                                                                                                                                                                                                                                                                 Venkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
sumain parotid gland.";
EMBL/GenBank/DDBJ databases.
EMBL, AF432917: AAL28113.1;
SEQUENCE 249 AA; 27110 MW: FD54B624AlA4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLJLDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVT!FTDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GENESFPVTANVTVAGPIIGQIINEKASEDELFAVTIETDPQTHQPVAVERECASDPTSI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SLSLLDKHSQIINKFVNSVINTLKSTVSSILQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
182 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEJCPLIRIFIHSLDVNVIQQVVDNPQH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LQLWKLVLLCGVLTGTSSLLDNI,GNDLSNVVDKLEPVLHEGI,ETVDNTLKGTLEKL,KVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata: Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                       99.3%; Score 1220; DB 4; Length 249; 99.6%; Pred. No. 1.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                          PRT;
                                                                                                                                                                                           PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KTQLQTL1 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 KTQLQTLI 249
                              241 KTQLQTLI 248
                                                       242 KTQLQTLI 249
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_TaxID=9913;
                                                                                                                                                                                                                                                                                       TISSUE=PAROTID;
                                                                                                                        Q96DR5
Q96DR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P79124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P79124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m
                                                                                                ESULT
96DR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \ESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ڡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ∑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ≿
    Ω
                              \succ
                                                       Ω
                                                                                                                           O O F F F B & O O O X X B O K F F F F K S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ≥-
```

```
Haigh B.J., Wilkins R.J., Wheeler T.T.; "The cloning and sequencing of two cDNAs coding for alternate forms of WSP30, a bovine member of the Parotid Secretory Protein family."; submitted (NOV-1966) to the EMBL/GenBank/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 ---LESRCSDEVVEQ--QETENFLEQLISRIFQVVSRLTGVRIRNVQVPDITFEATSENS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GLNLSFPVTANVTVAGPIIGQTINLKASLOLLTAVTIETDPQTHQPVAVLGECASDPTST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 A-DVSIPITADVTVSLPLLGEIVKLDLNVDLQTSVSIETDAETGDSRVVVGECPNNPESI 173
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 1.QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQLWKLVLLCGLLAGTSASLPDIRGND---VLRKLKSGLERGLDTFDSTIEIIFQNLKTE 58
                                                                                                                                                                                                                                                                                                                                                                              1 LQLWKLVILCGVLTGTSESLLDNIGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKI.KVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VOLWKLVLLCGLLAGTSESLLDIRGND---VLRRLISGLERGLGTFDSTIEI1FQNLKTE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
BSP30, a bovine member of the Parotid Secretory Protein family."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U79413; AAB38282.1; SEQUENCE 243 AA: 26877 MW; OC2D8DD45660E11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
                                                                                                                                                                                                                                                                                                          ..
æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 415.5; DB 6; Length 240; 37.9%; Pred. No. 7.8e-23; tive 56; Mismatches 84; Indels 11;
                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.6%; Pred. No. 2.16-24;
Matches 95; Conservative 58; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U79414: AAB38283.1; -. SEQUENCE 240 AA; 26513 MW; 850611DE9E43E358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = - = :: = :: = ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 37.9°
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
```

RESULT

qq ò g

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                        Rattus norveqicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirels L., Ball W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98129760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                     multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMGB1/SMGB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q63550-
Q63550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            063590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
               Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CSTBL/63; TISSUE-TONGUE;

X RADIATE-27085660; PubMed=11217851;

X RANAWA T., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arakawa T., Hara A., Fukuhishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Alzawa Y., Bata A., Ashburner M., Batalov S., Yamanaka I.,

X Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,

X Radia K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aon H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Wang K., Wawaji H., Kohtsuki S.,

M., Wang K., Washida K., Rasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.
171 SLTVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDAECVEKLIGESQD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFG--LKISNSL1LDVKAEPIDDGKGLN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 QATSWPLAKNSILET---LNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSSNGNGID 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LVVLCGLLIGNSESLLGELGSAVNN------LKILNPPSEAVPQNLNLDVELLQ 54
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse CDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 LLDKHSQIINKFVNSVINTLKSTVSSLLQKEJCPLIRIFIHSLDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 LLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSVLQGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.7%; Score 352.5; DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AA; 24737 MW; A29D0160268DA0CF CRC64;
                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; Pred .v. +ive 62; Mismatches
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK009654; BAB26418.1; -.
MGD; MGI:97787; Psp.
SEQUENCE 235 AA; 24737 MW;
                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Conservative
                                                                                                                                                                                                                                                                                                      PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                         241 KTQ 243
                                                                                                231 TTQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                       Q9D734;
                                                                                                                                                                                                 09D734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          063471
                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
```

Matches

ô g ó g ŏ g δ g Q63471 ID Q0

```
Mirels L., Ball W.D.;
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy
protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GSLQQATTWPSAKDSILET---LNXV--ELGNSNGFTPLNGLLLRVNKFRVLDLQAGLSS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 DKISISLLGRRLPFVNRILDGVSGLLTGAVSILLQNILCPVLQYLLSTWSGSAIQGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG--LKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLI.TAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 NGKDIDLKLPLVFE1SFSLPV1GPTLDVAVSLDLINSVSVQTNAQTGLPGVTLGKCSGNT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 TSISESELLDKHSQIINKFVNSVINTLKSTVSSELQKEICPLIRIFIHSEDVNVIQQVVDN 237
                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QLGSLVVLCGLLIGTSESLLGDVANAVNN------LD11LNSPSEAVAQNLNLDV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEONATAL SUBMANDIBULAR GLAND PROTEIN. 0B36EC779025986E CRC64;
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.0%; Score 331.5; DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mirels L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PEECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-92129360; Pubmed-1370829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-92129360; PubMed=1370829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 267:2679-2687(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIĞNAL 1 20 PC
CHAIN 21 235 N
SEQUENCE 235 AA; 24529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 330:437-444(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M83209; AAC06334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.7%;
```

```
5 WTFTLLCGLLAATL...--PKVIKEKI.TOEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 AA; 52373 MW; 377DBFA5E736709B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 DPTSISLSLI,DKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 NESTERUSLUHKUSFVVNSLAKNVMNLLVPALPQIVKNHLCPMIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310074B19R1K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) VON EBNER MINOR SALIVARY GLAND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Mismatches
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U46068; AAA87581.2; -.
InterPro: PRROIL24; LBP_BPI_CETP.
SMART; SM00328; BPI1; 1.
SMART; SM00329; BPI2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SWISS-WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                        (Wouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                 217 QLV 219
                                                                                                                                                                                                                     232 QQV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9D6P2
                                                                                                                                                                                                                                                                                                                          961114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
Q9D6P2
                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID AC DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                      οy
                                                                                                                                                                                      q
                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 òγ
                                                              q
                                                                                             ò
                                                                                                                           a
                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 NGDEVTEKMPMALNASE, SLPARDLTTDVSISMEATTSFALEKDPKTGRRVLNMQRCSENT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 TSISLSLLDKHSQ11NKFVNSV1NTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 237
 "Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  58 KVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 DGKGLNLSFPVTANVTVAGPIJGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9%; Score 159; DB 4; Length 484;
Best Local Similarity 23.9%; Pred. No. 0.00098;
Matchis 58; Conservative 48; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                         47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 OLGSLVVLCGLLIGTSGSLFDIFONPELDVESVWSEINYRIRYALETMDLDMLADYLSKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QLWKLVLLCGVI,TGTSESLLDNLGN---DLSNVVDKI,EPVLHEGLETVD-NTI,KGILEKL 57
                                                                                                                                                                                                                           NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          16.9%; Score 207.5; DB 11; Length 206; 24.0%; Pred. No. 9.6e-08;
                                                                                                                           Mirels L., Miranda A.J., Ball W.D.; "Characterization of the rat salivary-gland Bl-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMHLRE). 19, Created)
01-DEC-2001 (TrEMHLRE). 19, Last sequence update)
01-DEC-2001 (TrEMHLRE). 19, Last annotation update)
01-DEC-2001 (TrEMHLRE). 19, Last annotation update)
SIMILAR TO DNA SEGMENT, CHR 2, MASSACHUSETTS INSTITUTE OF
                                                                                                                                                                                                                                                                                                                                         84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC008429; AAH08429.1; -. EMBL; BC008429; AAH08429.1; -. FUNTIENCE 484 AA; 52427 MW; 08242B697284E858 CRC64;
                                                                                                                                                                                                                                                              91C001620761067B CRC64;
                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                         53; Mismatches
                                                                                                                                                                                                                     PUTENT LAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR'I';
                                                 Biol. Chem. 267:2679-2687(1992)
                                                                                                                                                                       Biochem, J. 330:437-444(1998).
EMBL; M83210; AAC12783.1; -.
                                                                                                                                                                                                                                                              206 AA; 23027 MW;
                                                                                                                                                                                                                                                                                                                                           58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                     20
206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                             MEDLINE=98129760;
                                       multigene family.
                                                                                                                                                                                                                                2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TECHNOLOGY 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 PQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PQ 201
                                                                                                                                                           proteins."
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96HK6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096HK6
                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396HK6
                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEEDZAOX 4 HEDRX FEFFO
                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ≥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ≻
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ≥
```

```
57 I.KVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLI.PTNTDIFGLKISNSLILDVKAEPI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 DDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAV-LGECAS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 TYNQELVVRIPLDMVAGLNTPLIKTIVEFQMSTEVQALIRVERSKS--GPAHLNLSDCSS 159
                                                                                                                                                                                                                                                                                                102 SANDQELLVKIPLD---MVAGFNTPLVKTIVEFHMTTE--AQATIRMDTSASGPTRLVLS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 DCATSHGSLRIQLLHKLSFLVNALAKOVMNLLVPSLPNLVKNQLCPV1EASFNGMYADLL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 LPL-LRAMODKSG-----SIPILDSFVHTVLKY---IIWMKVTSANILQLDVQPS 101
62 -----GVIQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                     116 IDDGKGLNLSFPVTANVTVAG---PIIGQIINLKASLDLLTAVTIETDPQTHQPV-AVLG 171
                                                                                                                                                                                                                                                                                                                                                                                                172 ECASDPTSISUSLIDKHSQ11NKFVNSV1NTLKSTVSSLLQKEICPL1RIF1HSLDVNVI 231
                                                                                                45 KDHNATSILQQLPLLSAMREKPAGGIPVLGSLVNTVL---KHVIWLKVITANILQLQVKP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snead M.L., Villanueva J., Paine M.L., Lei Y.P., Zhu D.H., Lusis J., Xia Y.-R., Yang J.-N.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WKLVLLCGVLTCT----SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WITTLICGLIGATLVQANVYPPAVL-NLGPEV-----IQKHLTQALKDHDAT--AJLQE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 150.5; DB 11; Length 474; 23.1%; Pred. No. 0.004;
```

```
CSTRAIN-C57BL/61; TISSUE-TONGUE;

RX MEDLINE-21085660; PubMed-11217851;

RA Arawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kochimi L., M., Staubi F., Suzuki R., Tomita M., Hanger L., Washio T.,

RA Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustinctch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Warshiazaki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSPPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 LELSVKLDVTAEVYAVRDSYGRSKL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 VLGKVISS-IPLENNILDIRVINPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=TONGUE;
REDLINES-21865660; PUDWEd=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 148.5; DB 11; Length 235; 25.3%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MACHINE AUGUSTA BABZE728.1; -. MGD; MG101143; BABZE728.1; -. MGD; MGI1919687; 2310074B19Rik. SEOUENCE: 235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT: 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2310021H06RIK PROTEIN.
                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310021H06RIK.
2310074B19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09D794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                            0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

```
A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S., A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asaito T., Okazaki Y., Gojobori T., Bono H., Batalov S., Casavant T., Asatota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Conchwa H., Ashburner M., Batalow B., Rochiwa H., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brash G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ashburner C., Fujita M., Gariboldi M., Andrewstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ashrons P., Marchlonni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Savaki H., Sato K., Schoenbach C., Walttaker C., Whittaker C., Whittaker C., Whittaker C., Whittaker C., Whittaker V., Wayashiya V., Narabiya V., Kawaji H., Kohtsuki S., Narabiya V., Kawaji H., Kohtsuki S.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T., Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M., Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshelbert S., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIJGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Subaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Kodentia; Sciurognallii; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.3%; Pred. No. 0.0027;
Matches 39; Conservative 38; Mismatches 74; Indels 3:
                                                                                                                                                                                                                                                                                                                                                           FULLE 409:685-690(2001).
EMBL; AK009441; BAB26290.1; -.
MGD; MGI:1914385; 2310021H06Kik.
emonikuce 270 Aa; 29223 MW; DB63327561D910AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 LTRVIPGLVOGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_Tax1D-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2310021H06RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09C0X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09C0X3
                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
```

Wed Aug

```
232 AA; 25713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 21.1% Matches 55; Conservative
                                                                                                                      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700058C13RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1700058C13RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                  Query Match
                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909093
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                909099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., A Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., A Arakawa T. Hara A. Fukunishi Y., Kondo H., Adachi J., Fukuda S., A Aizawa K. Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Kadota K., Matsuda H.A., Ashburna M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburna M., Batalov S., Casavant T., Kuhl P., Lewis S., Matsud Y., Ashburna M., Pasalos G., Quackenbush J., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washia Y., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washia T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Redriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilming L., Walman R.H., Weitz C., Wilming L., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 JNLKASLDLLTAVT1ETDPQTHQPVAVLGECASDPTSISLSLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29235 MW; A86F02ABBAAFBCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                29175 MW; 492A16EEBAB4A677 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310021H06R1K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148.5; DB Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 LTRVIPGLVQCVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 LKSTVSSLLQKELCPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Mismatches
Nature 409:685-690(2001).
EMBL; AK010115; BAB26710.1; -
EMBL; AK009239; BAB26221.1; -
EMBL; AK009531; BAB26343.1; -
EMBL; AK009562; BAB26360.1; -
EMBL; AK009580; BAB26772.1; -
EMBL; AK009595; BAB2640.1; -
EMBL; AK009803; BAB2644.1; -
EMBL; AK009803; BAB2644.1; -
EMBL; AK009803; BAB2644.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK010145; BAB26730.1; -.
MGD; MGI:1914385; 2310021H06Rik.
                                                                                                                                                                                                                                                                                                                         EMBL; AKO10051; BAB26667.1; -.
MGD; MGI:1914385; 2310021H06KiK.
SEQUENCE 270 AA; 29175 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE-TONGUE;
                                                                                                                                                                                                                                                               AK009835; BAB26533.1; -. AK010012; BAB26642.1; -. AK010051; BAB26667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2310021H06R1K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
               LERKKKKKKKKKKO
```

```
ACCOUNTE TO NOTE TO STANDARY TO STRAIN CONTROL TO STRAIN CONTROL TISSUE TESTIS;

MEDLINE-21085660; PubMed=11217851;

R Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

R Arakawa T., Hara A., Fukuhishi Y., Konoo H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Riyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Staubli F., Suzuki R., Tomitra M., Magner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomitra M., Magner L., Washio T.,

RA Sakai K., Okido T., Frunno M., Anno H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Somstein M. J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schopata T., Shibata Y., Storch K.-F.,

RA Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                              83 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVOSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                       143 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 132; DB 11; Length 232;
21.1%; Pred. No. 0.036;
tive 54; Mismatches 88; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 KG-----ILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 EGRIQSMRLLDRLNVSGTVAPGMVGWLIGGMNFQQQQEISINI----TNVQL---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LWK-LVLLCGVLT------GTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTL 50
                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LWRLLVLLLGLLALPSALPKQPWPGLTXAHKDGRST-----LARIIAQGLLKLN--A 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
11.8%; Score 145.5; DB 11; Length 270; 25.3%; Pred. No. 0.0045; Live 38; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0D52D24A3076D5DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AK006829; BAB24760.1; ...
MGD; MGI:1920638; 1700058C13Rik.
```

./ 105 NSLILDVKAEPIDDGKGLNLSFP---VTANVTVAG------PIIGQIINLKASLDLLTAV 155

```
62 -----GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 SANDQELLVKIPLD----MVAGFNTPLVKTIVEFHMTTE--AQATIRMDTSASGPTRLVLS 156
102 -------DCGCIQMAFPKEWFSANITLEFDIEFKLPFNSNIIKTHACMGLTAES 148
                                                                                                                                                156 TIETDPQTHQPVAVLGECASDPTSISLSL-LDKHSQIINKFVNSVINTLKSTVSSLLQKE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 KDHNATSILQQLPLLSAMKEKPAGGIPVLCSLVNTVL---KHILWLKVITANILQLQVKP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 IDDGKGUNI,SFPVTANVTVAG---PIIGQIINI,KASLDLLTAVTIFTDPQTHQPV-AVLG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 WTFTLLCGLLAATL------IQATLSPTAVLILG------PKVIKEKLTQEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WKLVLLCGVLTGTSESLLDNLCNDLSNVVDKLEP--VLHEGLETVDNTLKGILEKLKVDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
BA49C10.6 (SIMILAR TO MURINE VON EBNER MINOR SALIVARY GLAND PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 10.5%; Score 129; DB 4; Length 199; Best Local Similarity 24.2%; Pred. No. 0.049; Matches 54; Conservative 40; Mismatches 89; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracey A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121901; CAC03550.1; -.
NON_TER 199 199
SEQUENCE 199 AA; 21517 MW; 49A4CC2143BE04B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|: | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     215 ICPLIRIFIHSLDVNVIQQVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1111 : (11 ::: :1
208 VCPLIGEILRQLDVKLLKGLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09BQP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09B0P8
                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: August 6, 2002, 17:09:28 Job time: 930 sec

```
(without alignments)
198.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human parotid secr
Human parotid secr
Human PRO1025 prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequ
Peptide #8941 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expres
Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #9264 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 28.6 kDa sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AB1990.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1994_DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDS1/gcgdata/hold-geneseq/genesecp-embl/AA1986.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1993.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/qcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SlDS1/gcgdata/hold-geneseg/geneseqp-embl/Aa1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
                                                                                                                                                                                                                                                1 LQLWKLVLLCGVLTGTSESL......NVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:
                                                                                                                     August 6, 2002, 16:52:51; Search Lime 138.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                      US-10-020-139-2_COPY_2_249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM35227
AAE05367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW60682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB25765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM25745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB41435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM62308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM75111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB7535
                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 daximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1000.0
1000.0
1000.0
1000.0
200.0
200.0
150.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110...
111...
111...
112...
112...
12...
12...
12...
12...
12...
                                                                                                                                                                                                        Fitle:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228
1228
1228
1228
1228
1190
246
246
246
189.5
                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jatabase :
                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                  sednence:
                                                                                                                        ₹un on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (esult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
```

	183.55 183.55 183.55 183.55 16	1111		വ	22	AAY69164 AAU39019 AAU29210		DISCUSSION COLEA
	5 183 8 183 9 183 0 183 2 1							Human secrete
H H (4 (4 (4 (4 (4 (4 (4 (4 (4 (4 (4 (4 (4	8 183 9 183 0 183 1 1	1		S	7 7			Human PRO poly Human polypep
(4 (4 (4 (4 (4 (4 (4 (4 (4	0 183 1 1 2 1			9	22			Human LUNX pro
4 : 4 : 4 : 4 : 4 : 4 : 4 : 4	7 7	, 1	-	90	22			Human polypep
4 (4 (4 (4 (4 (4				000	777			Human digesti
1 (4 (4 (4 (4	η	٠.		7 -	77			Human NOV6h p
4 (4 (4	· CT ·			00 (21			Human neurotra
(4	7	7		သေ	22			Amino acid sec
(4				ထေ	21			Human PRO1357 Human PRO pol)
(*) (*	0.	~ ~		000	22			Human PRO1357
1 (*) (4		000	21			Human secreted pro
) (n 4			7 5	22			Lung cancer as
1 (*)				82	22			Staphylococcus
(*) (*)	7				17			C. difficile (
(*)				02	22			Staphylococcus
(r) -Q	00			15	22			Staphylococcus Recombinant er
. 4.				8 1	17			Recombinant er
ক ব	2.6			0.5	22			Amino acid sec
' ব' ব'	4 E		10	679	22 15			Haemophilus influ Tobamovirus repli
						ALIGNMENT	STA	
RESUL AAW69 ID	JT 1 9221 AAW69221	stand	tandard;	Prote	in;	249 AA.		
ž ų	AAW69221;							
ŏ F	4	a	 	4	;			•
: X	1-170-01	o n	rirst)	encr	۲ ک			
E 2	Human par	otid	secre	tory	prot	ein.		
X	Parotid s non-immun therapy;	ecre e de diag	tory presentations for the second sec	protein ve disc	in; hP. sorder	SP; diges ; immune	tive disorder; system disorder	endocrine disord ; cancer; human;
SS	Homo sapi	ens.						
5 H. E.	Key Peptide		1.	.T. m	na	fiers		
555	Ω,		/note 19	1 4 5 1 4 9	"signa "matur	l peptide e hPSP"	£	
೮೭೮	WO9828420	-A1.	1					
0.3	02-JUL-19	98.					•.	
<u> </u>	18-DEC-19	97;	9.7WO	-0823	522.			
5 E :	23-DEC-19	96;	9608	-0034	429.			
××	(HUMA-)	HUMAN	GENOME	E SCI	INC			
ž t	Duan P.	41.9	Ψ.					

```
amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hSSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence is the human parotid secretory protein (hPSP) of the
                                                                                                                                                                  nucleic acid encoding human parotid secretory protein or its gments - useful for diagnosis and treatment of, e.g. digestive endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hPSP-binding proteins.
WPI; 1998-377651/32.
                                                            N-PSDB; AAV44759
```

249 AA; Sequence

```
121 GLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                     181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFJHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                    0; Gaps
                                                                                                     1 LOLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                2 lqlwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkvd 61
100.0%; Score 1228; DB 19; Length 249; 100.0%; Pred. No. 2.3e-100; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW60682 standard; Protein; 249 AA.
                                                      Matches 248; Conservative
                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KTOLOTEL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 ktglqtli 249
        Query Match
```

```
Query Match 100.0%; Score 1228; DB 19; Length 249; Best Local Similarity 100.0%; Pred. No. 2.3e-100; Matches 248; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB24069 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                     241 KTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                   242 ktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                   a
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                  ga
                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                    ô
                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                    ô
```

Parotid secretory protein; human; cancer; autoimmune disease; secretory tissue; gastrointestinal lissue; HPSP; Siorgen's syndrome; draves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.

WO9821329-A1

Human parotid secretory protein (MPSP).

18-SEP-1998 (first entry)

```
screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, Graves disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purification of HPSP from natural sources. Expression of HPSP may indicate cell proliferation. HPSP nucleic acid or its fragments are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTUFFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SLSLLDKHSQJINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LQLWKLVLLCGVLTGTSESLLDNJGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 Iqiwkivilcgvltgtseslidnigndlsnvvdklepvlhegletvdntlkgileklkvd 61
                                                                                                                                                                                                                                                                                            treatment of cancer
                                                                                                                                                                                                                                                                                        New parotid secretory protein - useful for, e.g. treat and auto-immune disease, particularly of secretory or gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1A-C; 65pp; English.
                                         97WO-US20651.
                                                                                       96US-0749288.
                                                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                            Sandman O, Goli SK;
                                                                                                                                                                                                                      WPI; 1998-297933/26.
                                                                                                                                                                                                                                                 N-PSDB; AAV37699
                                         07-NOV-1997;
                                                                                  14-NOV-1996;
22-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
```

- A TABLESTA

1 LOLWKLVLIGGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60

```
ò
                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO30, PRO31, PRO109, PRO619, PRO109, PRO219, PRO2
                                                                                     Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard A, Gurney AL, Hillan KJ, Roy MA;
                                                                                                                             proliferation; tumourigenesis; identification; cancer; cytostalic; monostropic, neuroprotective; antiinfammatory; immunosupressive; immunostimulant; antiaquigenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; plandular disorder; macrophagal disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer \cdot
Human PRO1025 protein sequence SEQ 1D NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US28313.
99WO-US30911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US05028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0143048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-2000; 2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US12252
99US-0141037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker KP,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200053755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1999
```

```
chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; eye disorder; cobesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87725-A87774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the CDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The CDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted
                                                                                                                                                      Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                       61 I.GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                            121 GLNLSFPVTANVTVAGPIIGOIINLKASLDLLTAVTJETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                             181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                  2 lqlwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgilekikvd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB25765 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein SEQ ID #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-IB02058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980S-0113686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bougueleret L, Dumas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  septic shock; impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping procedures -
                                                                                                                                                                                                                                                                                       241 KTQLQTLI 248
                                                                                                                                                                                                                                                                                                                            242 ktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA87727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200037491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB25765;
                                                                                                                                                                                                                                                                                                                                                                                                      AAB25765
                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

Gaps

100.0%; Score 1228; DB 21; Length 249; 100.0%; Pred. No. 2.3e-100; tive 0; Mismatches 0; Indels 0;

Conservative

248;

Local Similarity

Query Match Matches

the present invention.

Sednence

.. 0

```
therapy and chromisome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.
proteins. The cDNAs may also be useful in diagnostic, forensic, gene
```

Sednence

Ouery Match Best Local S

Matches

```
WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                               248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM25745;
                                                                        Sequence
                                                                                                                 Query Match
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM25745
                                                                                                                                                                                                                                                                                                                                                                                   qq
00000x0
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                        (21 GLALSFPVTANVTVAGPIIGQIINLKASLBLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                 2 Iqlwklvilcgvitgtsesildnigndisnvvdklepvlhegletvdntlkgileklkvd 61
                                                                                                                                                                                                                                                 1 LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                     100.0%; Score 1228; DB 21; Length 249; 100.0%; Pred. No. 2.3e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75351 standard; protein; 249 AA
                                                                                                                                                                                                                   0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2000; 2000WO-1800951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     Local Similarity
                                                                                                                                            249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KTOLOTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 ktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100806-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JAN-2001.
                                                                                                                                                                                                                   248:
```

49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples -

Claim 10; Page 281; 307pp; English

Jobert S;

Dumas Milne Edwards J, Bougueleret L,

infection

AAB75351;

.B75351

WPI; 2001-071487/08

```
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; contral nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiagqregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
                                                                                                                                                                                                                                                                                                                                                                              61 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GLALSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 glnlsfpvtanvtvagpiiggiinlkasidlltavtietdpqthqpvavlgecasdptsi 181
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                 1 LQLWKI,VLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                                                                                                                          2 Jqlwklvllcgvltgtseslldnlgndlsnvvdklepvlhegletvdntlkgileklkvd 61
The present invention relates to 49 Secreted proteins and the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                    encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                      .
                                                                                                                                                                                      100.0%; Score 1228; DB 22; Length 249; 100.0%; Pred. No. 2.3e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (first entry)
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorder.
                                                                                                                                                                                                             Local Similarity
                                                                                                                 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ktglgtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, theumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    central nervous system; Virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antiulier; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, neurological disorders. Parkinson's disease, neurodegenerative and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM295963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGVLQKSSAWQLAKQKAQEAEKLLNNV1SKLLPTNTDIFGLKISNSLILDVKAEPIDDGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GLNLSFPVTANVTVAGPIIGQIINLKASUDILLTAVTIETDPQTHQPVAVIGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. LQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1190; DB 22; Length 260;
Pred. No. 5.5e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB41435 standard; Peptide; 50 AA.
Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 241; Conservative
                                                                                                                                                        2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 ktglqtli 260
                                                                                                                                                                                                                                                           N-PSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB41435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \BB41435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ă
                                                                                                                                                                 \overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\vdash}\overset{\times}{\vdash}\overset{\times}{\times}\overset{\times}{\otimes}\overset{\times}{\times}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}\overset{\times}{\cup}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ≿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ⋩
```

```
Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ 1D NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.1e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM62308 standard; Protein; 50 AA
                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456. 30-JUN-2000; 2000US-0608408.
                                                                                          30-JAN-2001; 2001WO-US00669.
                                                                                                                                 04-FEB-2000; 2000US-0180312.
                                                                                                                                                                                                        21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                     2000US-0608408
                                                                                                                                                                                        03-AUG-2000; 2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157275-A2.
                WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO Sapiens
                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                       30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM62308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM62308
```

```
Score 246;
                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                   20.08; Scor.
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                   AAM35227 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-0CT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001 (first entry)
                                                                                                                                                                                                                Best Local Similarity 100.
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488897/53.
                                                                                                                                                     50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                  AAM35227;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                               × 8 × 0 0 0 0 0 0 0 × 8
                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                          present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human yenome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                             Example 4; SEQ 10 NO: 34413; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                          20.0%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 1.1e-14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human bone marrow -
                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM75111 standard; Protein; 50 AA.
                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                           04-OCT-2000; 2000GB-0024263;
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                  the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0632366.
2000US-0234687.
                           2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0236359,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                   WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                               50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
             21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                             27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULT
M75111
```

```
0
                                                                                                             probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and dissplaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #9264 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                          The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
Example 4; SEQ 1D NO: 35417; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 246; DB 22;
Pred. No. 1.1e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
```

DB 22; Length 50;

. 6

```
The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell indiration of and proliferation. Cell-cell interaction and the differentiation of the differentiation of the discussion of the maintenance of tissue-specific cell-cell interaction and the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise attibodies, to isolate corresponding interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response the analysis of are useful for promoting immune response
                                                                                                                                                                                                                                                                                                                                                                                           Mouse, cytostatic; antiinflammatory, immunoregulatory, tissue integrity, wound healing, immune response, vaccine, caucer, asthma; allergy, cell trafficking, therapy, 28.6 KDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment, as immunoregulatory and anti-inilammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is 28.6 kDa protein, a secreted protein from mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -
                               Gaps
                               .;
0
                                                                      137 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLLLD 186
                                                                                             Indels
                             ..
           Pred. No. 1.1e-14;
100.0%; Prec. ....
                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 92; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                    Mouse 28.6 kDa secreted protein.
                                                                                                                                                                                                                      AAE05367 standard; Protein; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-017167B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2000; 2000US-0724864
                                                                                                                                                                                                                                                                                                         12-SEP-2001 (first entry)
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson JD, Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WP1; 2001-425665/45.
           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD10135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200148192-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2001
                                                                                                                                                                                                                                                                    AAE05367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                               Matches
                                                                                                                                                                                                    AAE05367
                                                                         ć
                                                                                                               g
```

```
115 gligkitssvplinnildikitdpgllelglvqspdghrlyvtiplgltlnvnmpvvgsl 174
                                                                                                                                                                                                                                              143 INLKASLDLLTAVTIETDPQ--THQPVAVLGECASDPTSISLSLDKHSQIINKFVNSVI 200
                                                                                                                                                      67 nptdllagkftdalsggl-----lsggl-----lgileniplldviksgggnsnglvg 114
                                                                                                                                                                                   86 NVISKL---LPTNTDIFGLKISNSI,ILDVKAEPIDDGKGLNLSFPVTANVTVAGP11GQI 142
                               Gaps
                                                                                                                       30 NVVD----KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLN 85
                                                                                         7 lvvlcgllahstaqlaglplplgqgpplplnqgpplplnqgqllplaqglplavspalps 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nh796_1. The sequence is predicted from a fuil-length cDNA clone (see AAX59356) isolated from a human adult brain (thalamus) cDNA library. The invention provides cDNA clones (see AAX59352-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel human secreted protein, termed
                               61;
DB 22; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; nh796_1; human; brain; thalamus; therapy;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "predicted leader/signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LaVallie ER;
                                                                                                                                                                                                                                                                                                        201 NTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                              231 giltkvlpeliggkvcplvngilsgldvtlvhniaellihglg 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted human proteins
                                                              6 LVLI,CGVLTGTSESLLD-------NLGNDL-----
                               49; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs K, LaVa
r RJ, Treacy M;
15.4%; Score 189.5; DB 2
23.3%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steininger RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06408 standard; Protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0070346.
              23,3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US27903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0222653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                             66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-419350/35.
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX59356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09935252-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06408;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                    AAY06408
                                                                                           q
                                                                                                                       δ
                                                                                                                                                      a
                                                                                                                                                                                                             q
                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                       δò
                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
```

TO STATE OF A STATE OF STATE OF THE STATE OF

```
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                             \overset{\circ}{\times} \overset{\circ}{\cup} \overset{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 KOKAQEAEKILINNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 kpgggtsggllggilgkvtsvipglnniidikvtdpgllelglvgspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 klqvntplvgasllrlavklditaeilavrdkgerihl-vlgdcthspgslqislldg1g 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 tglagsltnalsngl-----lsggl-----lgilenlplldil 77
encoding novel secreted proteins (see AAY06404-10) of the human testis, brain and foetal kidney. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, cytokine, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation or differentiation, immunostimulatant (e.g. as vaccine) or immunosuppressive, haematopoiesis regulating, tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 QI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 pipigglidsitgiinkvipelvggnvcplvnevirglditlvhdjvnmlihglg 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New LS170 nucleic acid from lung tissue – useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.9%; Score 183.5; DB 20; Length 256; Best Local Similarity 23.8%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth, activin or inhibin, chemotactic or chemokinetic, haemostatic, thrombolytic, receptor/ligand, antiinflammatory, cadherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colpitts TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dosen, Hodges SC, Klas
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US11601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0049183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Billing-medel PA, Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LS170 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Granadosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-060335/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX00809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts-rapp L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2SULT 1
```

```
9
                       contain at least on epitope in their sequences. The present invention relates to detection of a target LS170 polynucleotide that comprises the treating a test sample with at least one LS170-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LS170 gene. The LS170 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease. Specifically cancer, and to indicate predisposition to such disease. Particularly detection of LS170 polynucleotide, LS170 antigons, or anti-LS170 antibodies is indicative of disease. Cells transformed with an expression system comprising the LS170 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ab can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LS170-related nucleic acid can be used to isolate related sequences; as standards and reagents in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assays; as targets for drug screening, and as components or targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can used to deliver therapeutic agents to LSI70-expressing cells; directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KQKAQEAEKI,LNNVISK---LLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 kpgggtsggllggllgkvtsvipglnniidikvtdpqllelglvgspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 NYTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 klqvntplvqas]lrlavklditaeilavrdkqerihl-vlgdcthspgslqislldglg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 100; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 tglagsltnalsngl-----lsggl-----lsggl-----lgilenlplldil 77
Sequences AAW95463-471 represent LS170 polypeptide fragments which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 Q1-INKFVNSVINTLKSTVSSLLQKELCPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.9%; Score 183.5; DB 20; Length 256; Best Local Similarity 23.8%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of lung specific protein Lng110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY69164 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0095233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun Y, Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIAD-) DIADEXUS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200008206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [9-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY69164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69164
```

```
WP1; 2000-195589/17.
N->SDB; AA261165.
```

Lung specific genus for developing products for diagnosing, monitoring, staging, prognosticating, imaging and treating lung cancer

Example 2; Page 35-36; 37pp; English.

The present sequence is encoded by a lung specific gene, designated Lng110, clone ID 135520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer, especially metastatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for treating lung cancer.

Sequence 256 AA;

Query Match 14.9%; Score 183.5; DB 21; Length 256; Best Local Similarity 23.8%; Pred. No. 3.2e-08; Matches 56; Conservative 46; Mismatches 100; Indels 33; Gaps 6;

14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73

78 kpgggtsggilggtigktsvipginnlidikVtdpqlieiglvqspdgnilyvtipigl 13/ 13] NVTVAGPIIG-OIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189

SULT 15 (U39019

AAU39019 standard; Protein; 256 AA.

AAU39019;

16-JAN-2002 (first entry)

Human secreted protein nh796_1.

Human; secreted protein; antiinflammatory; immunosuppressive; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidabetic; virucide; antimifertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodefictency; SCLD; tumour; autoimmune disorder; multiple sclerosis; rhenmatoid archirits; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; Huntington's disease; infection; cardiac disease; stroke, sepsis; inflammatory bowel disease; contraceptive; immunogen; food supplement; vaccine.

Homo sapiens.

WO200175068-A2.

Search completed: August 6, 2002, 16:52:52

Job time: 334 sec

11-OCT-2001.

```
The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation activity or may induce production of other or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined continuous immune districtions and disorders e.g. multiple sclenois systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases of inflammation. The proteins are also useful in the treatment of diseases.

Condition of lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, inclsions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, amplotrophic lateral sclerosis, and Shy-Drager syndrome, infections, anylotrophic lateral sclerosis, and Shy-Drager syndrome, anylotrophic lateral periods and entral nervous system vessel e.g. stroke, anylotrophic lateral periods of processes of the peripheral periods of strains of the peripheral periods of cardiac and central nervous system vessel e.g. stroke, anylotrophic lateral periods of periods of cardiac and central nervous system vessel e.g. stroke, anylotrophic lateral periods of periods of the peripheral per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KQKAQEAEKLLNNVISK---ILPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 kpgggtsggllggllgkvtsvipglnniidikvtdpgllelglvgspdghrlyvtiplgi 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 NVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 klqvntplvgasllrlavklditaeilavrdkgerihl-vlgdcthspgslgislldglg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 tglagsltmalsng1-----1sgg1-----lgilenlplldil 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 OI-INKEVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 183.5; DB 22; Length 256; 23.8%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                    Lavallie E, Collins-racie LA, 1
7, Steininger RJ, Spaulding V,
Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 497–498; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                               30-MAR-2000; 2000US-0539330.
04-DEC-2000; 2000US-0729674.
                       22-MAR-2001; 2001WO-US09369.
                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                        Agostino MJ,
                                                                                                                                                                                                                                       Jacobs K, McCoy JM,
Treacy M, Agostino M
                                                                                                                                                                                                                                                                                                         Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639363/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS59237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                         Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
ò
```

```
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-6CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
                                                                                                                                         (without alignments)
118.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 6, Appli
Seguence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Appl
Sequence 2, Appli
Sequence 195, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98, A
Sequence 98, A
Sequence 98, A
                                                                                                                                                                                                                                       1 LOLWKLVLLCGVLTGTSESL.....NVIQQVVDNPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98,
                                                                                                                   August 6, 2002, 16:53:51 ; Search time 51.22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
1: Cggn2_6/Ptodate/2/laa/5A_COMB.pep:*
2: Cgn2_6/Ptodate/2/laa/5B_COMB.pep:*
3: Cgn2_6/Ptodate/2/laa/6A_COMB.pep:*
4: Cgn2_6/Ptodate/2/laa/6B_COMB.pep:*
5: Cgn2_6/Ptodate/2/laa/PcTUS_COMB.pep:*
6: Cgn2_6/Ptodate/2/laa/PcTUS_COMB.pep:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-915-136-6
US-09-541-782-10
US-08-431-517F-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-02465-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-480-604A-6
US-08-405-496A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-146-620-2
-09-395-453-2
                                                                                                                                                                                                                                                                                                                                           231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
                                                                                                                                                                                                  US-10-020-139-2_COPY_2_249
                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ű
                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq Length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2710
2710
2710
1057
481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                 OM protein
                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š.
```

Sequence 4, Appli Sequence 6, Appli Sequence 98, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 17, Appli Sequence 17, Appli Sequence 9, Appli		TREATMENT AND DISEASE
PCT-US94-06931-4 PCT-US94-07834-6 PCT-US95-00498-98 PCT-US95-00556-98 US-08-785-431-4 US-08-785-431-2 US-09-205-048-4 US-09-205-048-2 US-09-960-78-98-6 US-09-960-78-98-6 US-08-960-78-05 US-08-960-78-05 US-08-960-78-05 US-08-960-78-05 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-240-328-2 US-08-431-517F-17 US-08-431-517F-7	ALIGNMENTS	WITTOXIN FOR C. DIFFICILE SUITE 2200 PA SUITE 2100 #1.
44444444444444444444444444444444444444		Lication US/08480604A 130410N: KINK, JOHN A. THALLEY, BRUCE S. PENGA, JOSEPH R. STAFFORD, DOUGLAS C. ENTION: VACCIME AND A ENTION: VACCIME AND A ENTION: PREVENTION OF QUENCES: 32 CE ADDRESS: MEDLEN & CARROLL, LL 20 MONTGOMERY STREET, LIFORNIA UNITED STATES OF AMERI UNITED STATES OF AMERI ADBLE FORM: E: Floppy disk UNITED STATES OF AMERI ADBLE FORM: COMPATION: 42 ATION: 42 ATION: 42 ATION: 42 ATION: 42 ATION: 43 ATION: 43 ATION: 43 ATION: 43 ATION: 43 ATION: 44 ATION: 44 ATION: 44 ATION: 44 ATION: 44 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/40S, 4 E: 16 MAR-1995 ATION DATA: N NUMBER: US 08/329, 12 N NUMBER: US 08/329, 13 N NUM
		NESULT 1 US-08-480-604A-6 Sequence 6, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION: APPLICANT: RINK, JOHN A. APPLICANT: PRACA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: SAN FRANCISCO STREET: ZOO MONTGOMERY STREET, STREET; SAN FRANCISCO STREET: CALIFORNIA COUNTRY: UNITED STATES OF AMERIC CONFUTER FRAARABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/405,45 FILING DATE: US-UNIN-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/405,45 FILING DATE: L6-MAR-1995 FILING DATE: L
200000 000000 000000 00000 00000 00000 0000		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GG G G G G G G G G G G G G G G G G G G		SEGUENCE SEGUENCE OF PATCH NO. 5. PATCH NO. 5. PATCH NO. 5. APPLICANT STREET: CONTRESSON STREET: CONTRESSON STREET: CONTRESSON STREET: CONTRESSON STREET: CONTRESSON APPLICANT COMPUTE: COMPUTE

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      984 STSVKVQLY---AQLESTGLNTIYDSIQLVN----LISNAVNDTINVLPTITEGI---- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 -----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     927 ITKEISTIKNS11TDVNGNLLDN---1QLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                  48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG----- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TIETDPQTHQPVAVLGECASDPTSISLLCDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                      5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                             8.5%: Score 104: DB 1: Length 2710; 20.3%; Pred. No. 0.42; ative 63; Mismatches 109; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WILLIAMS, JAMES A.

TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECHONE: (415) 705-8110
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ 10 00: 6:
SEQUENCE CHARACTER (5TCS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08405496A Patent No. 5919665 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-1994
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-OCT-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 56; Conserva
                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                   ; MOLECULE TYP
US-08-480-604A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-405-496A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
```

```
Query Match 8.5%; Score 104; DB 2; Length 2710;
Best Local Similarity 20.3%; Pred. No. 0.42;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 ITKEISTIKNSIITDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSLIDYSSNKDVLNDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRACE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS.
APPLICANT: STAFFORD, DOUGLAS.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
APPLICATION NUMBER: US 07/429,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                        REGISTRATION NUMBER: 40.027
REFREENCE/DOCKET NUMBER: 0PHD-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Sequence 6, Application US/08915136
; Patent No. 6290960
                    FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                : 2710 amino acids amino acid
                                                                   NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                    inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94104
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                US-08-405-496A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-915-136-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
```

LENGTH: 1057

```
984 STSVKVÖLY --- AQLFSTGLNTIYDSIQLVN----LISNAVNDTINVLPTITECI----- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 20.3%; Pred. No. 0.42;
Matches 56; Conservative 63; Mismatches 109; Indels 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 LKVDLGVLQK-----SSAWQLAKQKAQEAEKLLN--NVISKLLPTNTDIFG---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807 KTLLLDASVSPOTKFILNNLKLNIESSIGDYIYYEKLEPVKNIIHNSIDDLIDEFNLLEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPITGOIINLKASLDLLJAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              927 ITKEISTIKNSI!TDVNGNLLDN---IQLDHTSQVNTLNAAFFIQSI.IDYSSNKLVLNL, 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KLVLLCGVLTGTSESLLDNLGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1032 -PIVSTILDGINLGAAIKELLDEHDPLLKKELEAKV 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 CPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFWMERE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: NISLOW, COREY
APPLICANT: SAKOWICZ, ROMAN
APPLICANT: BAROWICZ, ROMAN
APPLICANT: BETAUG, Christophe
TITLE OF INVENTION: Antifungal Assay
                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAK-1995
                                                                                                                                                APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             US 08/161,907
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET UMBER: OPT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                          APPLICATION NUMBER: US 08
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     incar
                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-541-782-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 OTHER INFORMATION: No. 6265187e: human LBP-b DNA and amino acid sequence US-08-431-517P-2
                                                                                                            8.1%; Score 100; DB 4; Length 1057;
24.4%; Pred. No. 0.26;
Live 34; Mismatches 79; Indels 70; Gaps
                                                                                                                                                                                                                                              447 LDOCKSDLONKTUELE------TTOKHLOETKLOL-VKEEYITSALESTEEKLH 493
                                                                                                                                                                                                                                                                                                                                         494 DAASKLLNIVEE----TIKDVSGLHSKLDRKKAVDOHNAEAQDIFGKNLNSLFNNMEELI 549
                                                                                                                                                                                                                                                                                                                                                                                                                           550 KDGSSKQKAMLEVHKTLFGNLLSSSVSALDTITTV------ALGSLTSIPENV 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 E-AEKLLNNVISKLLPTNTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF----- 126
                                                                                                                                                                                                                                                                                                                                                                                    127 ----PVTANVTVAGPIIGQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SL.SLLDKHSQIINKF------VNSVINTLKSTVSSLLQKEICPLIRIFIHSLD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 SIS-DSSIRVQGRWKVRKSFFKLQGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 IADVEVDMSGDFGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYIGTLPVTTEI 222
                                                                                                                                                                                                       21 LDNI,GNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQK--SSAWQLAKQKAQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VILCGVIJGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ILLALLITSTPEALGANPGL-VARITDKGLOYAAQEGLLALQSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Scott, Randal W
APPLICANT: Scott, Marian N
TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS
FILE REFERENCE: 1103/11307USO1
CURRENT APPLICATION NUMBER: US/08/431,517F
CURRENT APPLICATION NUMBER: 1995-05-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 96; DB 4; Length 481;
19.6%; Pred. No. 0.21;
ive 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 2, Application US/08431517F : Patent No. 6265187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ----NVIQQVVDNPQHKTQL 244
                                                                                             Overy Match
Best Local Similarity 24.4%
"***Thes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
TYPE: PRT
ORGANISM: H.sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-08-431-517F-2
                                           US-09-541-782-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 VN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 IN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
```

:: :|: |: |: 223 DSFADIDYSLVEAPRATAQM 242

qq

TITLE OF INVENTION: 123 Human Secreted Proteins FILE REFERENCE: P2010P1 CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08 CURRENT APPLICATION NUMBER: US/09/227,357 EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER FLING DATE: 1997-07-08 AFFLICATION DATE: 1997-0/-06
APPLICATION NUMBER: 60/051,916 FILING DATE: 1997-07-08
APPLICATION UNMBER: 60/051,919
APPLICATION NUMBER: 60/051,928
APPLICATION NUMBER: 60/051,928 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/052,732 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/051,918 FILING DATE: 1997-07-08 ICATION NUMBER: 60/051,920 NG DATE: 1997-07-08 FILLING DATE: 1997-07-08 APPLICATION NUMBER: 60/052,733 60/055,948 APPLICATION NUMBER: 60/055,949 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,950 APPLICATION NUMBER: 60/055,947 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/056,360 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,684 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/055,954 APPLICATION NUMBER: 60/052,803 APPLICATION NUMBER: 60/051,931 APPLICATION NUMBER: 60/051,932 ICATION NUMBER: 60/051,930 APPLICATION NUMBER: 60/052,795 ICATION NUMBER: 60/055,722 APPLICATION NUMBER: 60/055,723 APPLICATION NUMBER: 60/055,953 APPLICATION NUMBER: 60/055,964 FILING DATE: 1,997-08-18 APPLICATION NUMBER: 60/055,984 EARLIER APPLICATION NUMBER: 60/058,785 Sequence 195, Application US/09227357 Patent No. 6342581 GENERAL INFORMATION: 1997-07-08 1997-07-08 1997-07-08 1997-07-08 1997-07-08 1997-08-18 1997-08-18 FILING DATE: 1997-08-18 FILING DATE: 1997-08-18 1997-08-18 1997-08-18 FILING DATE: 1997-08 APPLICATION NUMBER: APPLICANT: Fischer et al. FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: 09-227-357-195 EARLIER A EARLIER I EARLIER I EARLIER I EARLIER I EARLIER A EARLIER
```
105 --NSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ANISLEFDLELRPSFD--------NIIKMCAHMSIVVEFWLEKDEF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LWKLVLLCGVLT-----GTSESLLUNLGNDLSNVVDKLEPVLHEGLETVDNTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LWRLLIFLGLLALPLAPHKQPWPGLAQAHRDNKSTLARIIAQGL--IKHNAESRIQNIHF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: White, Mark Leslie
APPLICANT: Garroll, Stephen Fitzhugh
APPLICANT: Ma, Jeremy Kam-kuen
TITLE OF INVENTION: METHOD FOR QUANTIFYING LBP IN BODY FLUIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 95.5; DB 4; Length 210; 19.2%; Pred. No. 0.069; tive 46; Mismatches 86; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 THQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,811
                                                                                                                                                                                                                                                                                                                                                                                      : LOCATION: (211)
; OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-195
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER PILING DATE: 1997-09-12
EARLIER PPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEO 1D NOS: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27129/31843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States of America
COUPER 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy.disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08186811
Patent No. 5484705
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy.disk
                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 19.29
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicago
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-186-811-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                         TYPE: PKT
                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                           FEATURE:
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 OKSSAWOLAKOKAORAEKLLNNVISKLI.PTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTLETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 SIS-DSSIRVQCHWKVRKSFFKLQGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 IADVEVDMSGDLGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYLQTLPVTTEI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ILLALLITSTPEALGANPCL-VARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                                                                                                                                                                                                                               7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cohen, Jonathan
APPLICANT: Mong, Ada H.C.
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                   7.7%; Score 94; DB 1; Length 481;
19.6%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSED: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6330 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/311,611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/08311611A
Patent No. 5523288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 ---- NVIQOVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 DSFADIDYSLVEAPRATAOM 242
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                              "rl.BP"
                                                                                                                                                                                                                                                                                                                                           19.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           : 481 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 19.6%
Matches 51; Conservative
                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                    OTHER INFORMATION:
US-08-186-811-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
Illinois
                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-311-611A-98
                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
```

```
SFPVTANVTVAG--PLIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 SIS-DSSIRVOGRWKVRKSFFKLQGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 HVGRG-------PREFHSLNIHSCELLHSALRPV-PGQGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 IADVEVDMSGDLGWLLNLFHNQJESKFOKVLESRICEMIQKSVSSDLQPYLQTLPVTTEI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Application US/08372783
Patent No. 5578572
GENERAL INFORMATION:
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 94; DB 1; Length 481;
19.6%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
                     NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                               REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ----NVIOOVVDNPOHKTOL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 DSFADIDYSLVEAPRATAOM 242
                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 98
                                                                                                                                                                                                                                                                                                                                                                  "rLBP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 481 amino acids
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature;
CTHER INFORMATION: "rLE
US-08-311-611A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 19.69
Matches 51; Conservative
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-372-783-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
```

```
STREET:
                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETU-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 IADVEVDMSGDJ.GWLI.NLFHNQJESKFQKVI.ESKT.CEMIQKSVSSDLQPYLQTLEPUTTET 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 HVGRG------PQGGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 SIS-DSSIRVQGKWKVRKSFFKLQGSFDVSVKG1S1SVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ÇKSSAWQLAKQKAQEAEKLLNNVISKLIPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VLICGVLTGTSESILDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 94; DB 1; Length 481; Best Local Similarity 19.6%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Little, Roger G.
APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewis H.
APPLICANT: Lambert, Lewis H.
APPLICANT: Scannon, Patrick J.
TITLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
                                                                                                                                                              NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENDE/DOCKET NUMBER: 27129/32415
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                  APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/08372105
Patent No. 5627153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F: Floppy disk
1BM PC compatible
                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 ----NVIQQVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 DSFADIDYSLVEAPRATAQM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: "rLBP"
US-08-372-783-98
FILING DATE: 11-JUL-1994
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 481 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-372-105-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
70 HVGRG------PQGGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 SPPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 SIS-DSSIRVQGRWKVRKSFFKLQUSFDVSVKGISLSVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 PTSISLSLLDKHSQIINKFVNSVIN----TJKSTVSSLLQKEJCPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 IADVEVDMSGDLGWLLNLFHNQ!ESKFQKVLESRICEMIQKSVSSDLQPYLQTLPVTTEI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VLLCGVLTGTSESLLDNLGNDLSNVVDK - LEPVLHEGLETVDNTLKGI - LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 7.7%; Score 94; DB 1; Length 481; Best Local Similarity 19.6%; Pred. No. 0.33; Matches 51; Conservative 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biologically Active Peptides from Functional Domains of Bactericidal/Permeability-Increasing Protein and
                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Allegretti & Witcoff, Ltd. Suite 3000, 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98, Application US/08306473A Patent No. 5562332 GENERAL INFORMATION:
APPLICANT: Little, Roger G.
                                                                                                                                        APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 08/209,762
                                                                                                                                                                                                                                                                                              08/183,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ----NVIQOVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 DSFADIDYSLVEAPRATAOM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "rLBP"
                                                                                                                                                                                                               APPLICATION NUMBER: 08/20 FILING DATE: 11-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              312/474-6300
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 481 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BY
TITLE OF INVENTION: FU
TITLE OF INVENTION: PO
TITLE OF INVENTION: US
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION:
US-08-372-105-98
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-306-473A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
```

```
US-08-261-660A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-209-762-98
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     òy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    op
Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 HVGRG------PGQGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 SFPVTANVTVAG--PIIGQIINLKASLDL-LFAVTIETD----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 SIS-DSSIRVOGRWKVRKSFFKLOGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPINTDIFCLKISNSLTLDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VLLCGVLTGTSESI.LDNLGNDLSNVVDK-I.EPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ILLALLITSTPEALGANPGL-VARITDKGLQYAAQEGLLALOSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
TITLE DE INVENTION: Lipopolysaccharide Binding Protein Derivatives
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

Ouery Match

7.7%: Score 94: DB 1; Length 481;
Best Local Similarity 19.6%: Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 107; Indels
                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateulin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   APPLICATION NUMBER: US/08/306,473A
                                                                                                                                                                                                                                                                                                                                                                                                                             93,1133-
                                                                                                                                                                                                                        FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        08/183,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/08261660A; Patent No. 5731415
                                                                                                                                                                                                                                                                                                                                                                                  NAME: McDonnell, John J. REGISTRATION NUMBER: 26,949 REFERENCE/DOCKET NUMBER: 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ----NVIQOVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 DSFADIDYSLVEAPRATAOM 242
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/20
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-715-1234
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312-715-1234
                                                                                                                                                                                                                                                                                 FILING DATE: 11-MAR-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
Chicago
                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-306-473A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-261-660A-4
                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
APPLICANT: Little, Roger G.

TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
TITLE OF INVENTION: Protein and Uses Thereof
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Pred. No. 0.33;
tive 52; Mismatches 107; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RYEFHSLNIHSCELLHSALRPV-PGQGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SFPVTANVTVAG--PITGQ11NLKASLDL-LTAVTIETD----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 SIS-DSSIRVQGRWKVRKSFFKLQGSPDVSVKGISISVNLLLGGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 JADVEVDMSGDLGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYLQTLPVTTEI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ILLALLLTSTPEALGANPGL-VARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 94; DB 1; Length 481;
19.6%; Pred. No. 0.33;
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27129/32137
                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUN-1994
CLASSFFICATION: 435
                                                                          Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 98, Application US/08209762
; Patent No. 5733872
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 ---- NVIQOVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 DSFADIDYSLVEAPRATAOM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: "rLBP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 19.6%
hes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312/474-630
TELEFA: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inear
                                                                                                                          60606-6402
          STREET: 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
```

```
APPLICANT: HOFWILS, Arnold H.

TITLE OF INVENTION: Method For Potentiating BPI Protein Bactericidal
TITLE OF INVENTION: Activity By Administration Of LBP Proteins
CORRESPONDENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 IADVEVDMSGDLGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYLQTLPVTTEI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 HVGRG------PYEFHSLNIHSCELLHSALRPV-PGGGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 PTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ILLALLLTSTPEALGANPGL-VARITURGLQYAAQEGLLALQSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 7.7%; Score 94; DB 1; Length 481; Best Local Similarity 19.6%; Pred. No. 0.33; Matches 51; Conservative 52; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/306,473
                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/08274303
; Patent No. 5770561
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 ----NVIQQVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 DSFADIDYSLVEAPRATAOM 242
                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 481 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                               90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-473-344-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-274-303-6
     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Little, Roger G
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
TITLE OF INVENTION: Protein and Uses Thereof
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

(), v., v., v., best Local Similarity 19.6%; Pred. No. 0.33;

Best Local Similarity 19.6%; Pred. No. 0.33;

Conservative 52; Mismatches 107; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 IADVEVDMSGDLGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYLQTLFFT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 QKSSAWQLAKQKAQEAEKLLNNVISKLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 HVGRG------PREFHSL/NIHSCELLHSALRPV-PGQGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD-----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SIS-DSSIRVOGRWKVRKSFFKLOGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 PTSISLSLLDKHSQ11NKFVNSV1N----TLKSTVSSLLQKEICPLLRIFIHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VLLCGVLTGTSESLLDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ILLALLLTSTPEALGANPGL-VARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIP 69
                                                                                                                                                                                                      SCHRARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/209,762
FILING DATE: 11-JAN-1994
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: No. 5733872nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,1133
                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/08473344 Patent No. 5763567
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-715-1234
TELEEX: 910-221-5317
INFORMATION FOR ESO 10 NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ----NVIQQVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 DSFADIDYSLVEAPRATAQM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: "rLBP"
US-08-209-762-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
Chicago
: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
                                                         USA
                                                                                                                                       MEDIUM TYPE:
                                                                                90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-473-344-98
                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

đ

δ qq ô

q δ q

δ g

```
Ouery Match 7.7%: Score 94; DB 1; Length 481;
Best Local Similarity 19.6%; Pred. No. 0.33;
Matches 51; Conservative 52; Mismatches 107; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 HVGRG-----PGGGLSL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 SFPVTANVTVAG--PIIGQIINLKASLDL-LTAVTIETD----PQTHQPVAVLGECASD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 SIS-DSSIRVOCKWKVRKSFFKLQGSFDVSVKGISISVNLLLGSESSGRPTVTASSCSSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 PTSISLSLLDKHSOLINKFVNSVIN----TLKSTVSSLLQKBICPLIRIFJHSLDV---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 QKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VLLCGVLTGTSESILDNLGNDLSNVVDK-LEPVLHEGLETVDNTLKGI-LEKLKVDLGVL 64
                    MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/274,303
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sharp Juffrey S.
REGISTRATION NUMBER: 31.879
REFERENCE/DOCKET NUMBER: 33157
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEFAX: 312/474-0408
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ----NVIQQVVDNPQHKTQL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 DSFADIDYSLVEAPRATAGM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: "rLBP"
US-08-274-303-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ολ
```

Search completed: August 6, 2002, 16:53:52 Job time: 284 sec

```
GenCore version 4.5 Copyright (c) 1993 · 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

August 6, 2002, 17:05:12 ; Search time 66.51 Seconds (without alignments) 310.618 Million cell updates/sec Run on:

US-10-020-139-2_COPY_35_249 Perfect score:

1 KLEPVLHEGLETVDNTLKGI.....NVIQQVVDNPQHKTQLQTLI 215 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched: 283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir3:* pir3:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	parotid secretory	parotid secretory	ibula	e-bisp}	a)		O	_	hypothetical prote	ical	probable invasin Z	- 24	hypothétical prote		1	calp	н	TI.	internalin protein	hypothetical prote	_	memb	probable ligand-bi	milý	hetical prot	ptina	A - Clostri	ved hypothe	fic meta
		ID	SOMS	3	A42337	A49943	S53378	9006	T50073	WMTM8T	D64505	H90975	E85822	D64182	T19148	B89944	557596	S37854	T30249	PC6003	AC1583	T27045	S64249	D64962	S17448	B82209	T18765	B82204	A37052	E82064	A60272
		DB	Н	7	7	7	7	7	7	Н	7	7	7	7	7	7	7	~	7	7	7	~	7	7	~	7	~	~	ď	~	~
		Length	m	3	0	Th.	S	n	72	_	21	-+	99	~	m	N	7.2	1038	93	62	m	_	10	\sim	\sim	-	S	7	71	S	99
ж		Match	~	4	14.6	0	0				9.5							8.8					٠	•			60				
		Score	94.	263.5	54.	0	0	ص	σ,	œ	97.5	9	9	95	95	4	4	93.5	ω.	66	σ	92.5	ζ,	g	91.5	65	91	16	91	90.5	0
	Result	. No !	-	7	3	4	S)	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

56 SKLLPTNTDIFG -- LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLK 113 114 ASLDLLTAVTTETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKST 173

3 EPVLHEGLETVDNTLK-----GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI 55

ò

ò qq ò a

	0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	88888899999999999999999999999999999999	თ თ თ თ თ თ თ თ თ თ თ ი 4 4 4 4 4 4 4 5 0 0 0	529 1056 2819 368 481 1075 1509 602		VGNZSP G02157 A90551 A11254 1156246 151557 B19985 B71562	cell fusion glycop kinesin-like spind conserved hypothet probable peptidogl lipopolysaccharide exportin 1 (valida Exportin 2 (XPO1) p hypothetical prote hypothetical prote
	4 4 4 4 4 4 4 5 4 5 4 5 4 5 5 5 5 5 5 5	87 . 5 87 . 5 87 86 . 5		990 6713 310 621 256 668	000000	C82759 B89921 P90011 T15859 S77810 139902	zinc proteinase XF hypothetical prote conserved hypothet hypothetical prote probable DNA topoi penicillin-binding
						ALIGNMENTS	
	RESULT SOMS parotid N'Altern C'Specie C'Date: C'Access	SQMS SQMS SQMS Parotid secretory protein prec N:Alternate names: PSP C:Species: Mus musculus (house C:Species: 31-Dec-1988 #sequence C:Accession: A23031; 153336	y protes: PSP usculus 988 #se	ein precus (house squence)	n n l	- mouse e) ion 31-Dec-1988	#text_change 22-Jun-1999
	Nuclei Color		J	, 1-13, 1-13, 1ing of 031; M	3, 1985 of mouse ; MUID:85	5 use PSP mRNA. :85215456	
S	400	ζ) ,	.01697; B.K.; 86		NID:953810; PIDN:CAA25846.1 Mikkelsen, B.M.; Harmark, K	1; PID:9758163 K.; Nielsen, J.T.; Hjorth,
		ع و مد	~ 2 2 2	murine 16, MUIL anslate	ne NUID ate	murine parotid secretory protein 6; MUID:87004556 anslated from GB/EMBL/DDBJ	and salivary amylase expr
A Casilla Casi	c;Comment C;Genetic	t: PSP is t	es: GB: s the m	GB:M26807 he most ab	nud Sund	GB:M26807; NID:9200556; PIDN:AAA40009.	.1; PID:9554264 d gland. Its function is n
	A.Gene: Psp A.Mar position: 2 A.Introns: 41/1 A.Note: list of introns m C.Superfamily: parotid sec C.Keywords: parotid dland F:1-20/Domain: signal seq F:21-235/Product: parotid	Gene: Psp Map position: 2 Introns: 41/1 Note: list of introns may be incomplet. Superfamily: parctid secretory protein Keywords: parctid gland; saliva 1-20/Domain: signal sequence #status p 21-235/product: parctid secretory prot	introns marchid sectid gland ignal seques	# C · · ⊃	be in etory saliva nce #s	y be incomplete retory protein saliva ence #status predicted <sig> secretory protein #status predicted</sig>	cted <mat></mat>
	Query Match Best Local Matches 6	Match ocal Simi s 69;	Similarity 9; Conser	vat	27.8%; 32.7%; ive	Score 294.5; DB 1; Pred. No. 2.8e-16; 55; Mismatches 74;	Length 235; Indels 13; Gaps 4;

```
fructose-bisphosphate aldolase (EC 4.1.2.13) - Staphylococcus carnosus (strain TM300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning, sequencing, and characterization of the gene encoding the class I A;Reference number: A49943; MUID:94042930 A;Accession: A49943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1995
A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1
A;Reference number: S53376
A;Accession: S53378
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Staphylococcus carnosus
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 15-Oct-1999
C;Accession: A49943; S33358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S53378; S56887; S57359
                                                                                                                       126 PKTGRRVLNMQRCSLNTDNTSISLLNRKSNFVNLALDSALYLIKRGLTLPVRRQLCPVLQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X71729; NID:9297873; PIDN:CAA50663.1; PID:9297874
C;Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 KGIVPFLKVDKGLAEEADGVQLMK-PIPDLDKLLDRA-----NERGIFGTKM-RSNILE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 NNKEAIE--KVVKOOFEVAKEIIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ----LLTAVTIET-----DPQTHQPVAVLGECASDPTSI3LSLUDKHSQ1INKF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 KKDQYVMLKLTIPTKVNAYSEL,IEHPQVIRVVALSGGYSRDEAN---KILKQNDGLIASF 260
                      66 LKIKULRILNLNHEVSPNGDEVTLKMPMALNASLSLPARDLTTDVSISMEAITSFAIEKD 125
                                                                                   128 POTHOPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: Z49384; NID: 91008292; PID: 91008293; MIPS: YJL109c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YJL109c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.0%; Score 106; DB 2; Length 296 Best Local Similarity 25.9%; Pred. No. 0.43; Matches 50; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R\text{:}Rasmussen, S.W. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1769 <RAS>
A;Cross-references: EMBL:X85021; NID:g728698; PID:g728701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N:Alternate names: hypothetical protein J0808
C:Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 175, 7495-7499, 1993
                                                                                                                                                                                                           188 JFIHSLDVNVIQQVVDNPQ 206
                                                                                                                                                                                                                                                                  186 LIISN---TFHPDEISNPO 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 VNSVINTLKSTVS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 SRALVSDLNAQQS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S56876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1769 <RAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-296 <WIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S56887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Witke, C.; Goetz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Rasmussen, S.W.
                                                                                                                                                                                                                                                                                                                                                                                            A49943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
                                                                                                                                              a
                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mirels, L.; Ball, W.D.
D. Blol. Chem. 257, 2679-2687, 1992
A:Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein ax
A;Reference number: A42337; MUID:92129360
                                                                                                                                                                                                                                                                                                                                                                                                                   A:Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein an
A;Reference number: A42337; MUID:92129360
A;Accession: B42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                        N;Alternate names: PSP
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #scquence_revision 03-Feb-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LKISNSLILLDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 --LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 LLLRVNKFRVLDLQAGLSSNGKDIDLKLPLVFEISFSLPVIGPTLDVAVSLDLLNSVSVQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 TDPQTHQPVAVI,GECASDPTSISLSLLDKHSQJINKFVNSVINTLKSTVSSLLQKEICPL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LETVDNTLKG1LEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TD1FG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 LDILNSPSEAVAONLNLDVGSLQOATTWPSAKDSILET---LNKV--ELGNSNGFTPLNG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Residues: 1-206 <MIR>
A;Cross-references: GB:M83210; NID:g206989; PIDN:AAC12783.1; PID:g206990
A;Note: sequence extracted from NCBI backbone (NCBIN:78707, NCBIP:78708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-215 cMIX-
A;Residues: 1-215 cMIX-
A;Cross-references: GB:NB3209: NID:g206456; PIDN:AAC06334.1; PID:g206457
A;Note: sequence extracted from NCBI backbone (NCBIN:78709, NCBIP:78710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%; Score 263.5; DB 2; 29.6%; Pred. No. 8.3e-14; tive 56; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 154.5; DB 2
24.5%; Pred. No. 3.6e-05;
Live 42; Mismatches 60
                                                          195 LSTVLONFLCPLIQYVLSTLNPSVLOGLLSN 225
174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: parotid secretory protein
                                                                                                                                                                                                              parotid secretory protein precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secretory protein
                                                                                                                                                                                                                                                                                                                                                                                         2679-2687, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submandibular gland protein A - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C: Keywords: parotid gland; saliva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 IRFFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 LOYLLSTMSGSA1QGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.5%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                               R; Mirels, L.; Ball, W.D. J. Biol. Chem. 267, 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-206 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Superfamily: parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                     C; Accession: B42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A42337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             òχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
   ò
                                                          QQ
```

6

.7 05:47:00 2002

Wed Aug

```
A:Molecule type: genomic RNA
A;Residues: 1-1615 COHN>
A;Note: readthrough of the terminator UAG between codons for Gln-1116 and Gln-1117 c
C;Superfamily: cucumber mosaic virus RNA 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1727 <MCD>
A;Cross-references: EMBL:AL133357; PIDN:CAB62414.1; GSPDB:GN00066; SPDB:SPAC1486.04<
A;Experimental source: strain 972h(-); cosmid c1486
                                                                                                                                                                                                                                                                                                                              Riohno, T.; Aoyagi, M.; Yamanashi, Y.; Saito, H.; Ikawa, S.; Meshi, T.; Okada, Y. J.; Biochem. 96, 1915-1923, 1984
A;Title: Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and A;Reference number: A91984; MUID:85157522
A;Accession: A04195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 30-Sep-1993 C;Accession: A04195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 KLQLDRLTNKFSSFCEQVKQRIPVVKQQRSEIVRNNIYMNFLSES-----LETSNNNLTK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 VKAEFIDDGKGLNLSF-PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 VQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSRNVPATVQ··VA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 LGECASOPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSL--D 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 LDEYAQNPSTASETLVNK--ELAN-----FSSIKEAVSKTLE-----LREKVRALECD 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 98.5; DB 1; Length 1615;
20.4%; Pred. No. 16;
.ve 44; Mismatches 79; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 KLKVDLGVLQKSSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIFGLKISNSL1LD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.4%; Score 99.5; DB 2; Length 1727; Best Local Similarity 26.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180K protein - tomato mosaic virus (strain L) N:Contains: 130K protein
                                    150 --SLLDKHSQIINKFVNSVINTLKSTVS 175
                                                                                                                      246 ANELLKDNDELIASFSRALASDLRADQS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: tomato mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: 225034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SPDB:SPAC1486.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 VNV100VV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 VEIQKOTV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T50073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Order of the cispecies of the cisp
R;Rasmussen, S.W. Yeast 11, 873-883, 1995
Yeast 11, 873-883, 1995
A;Teiten 377-5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3
A;Reference number: S57357; MUID:96090136
A;Accession: S57359
                                                                                                                                                                                                                                                                                 A.Residues: 1-1769 - RAF>
A.Cross-references: EMBL:X85021; NID:9728698; PIDN:CAA59385.1; PID:9728701
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-296 <KUR>
A;Cross-references: GB:BA000018; PID:913702563; PIDN:BAB43704.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SA2399 (imported) - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 KINIILSLIKK-----IRLERYEVRLIITDLIYLSEILEDKSQLVELFEYFISINEDLV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 JOVKAEPIDDGKGLNLSFPVTANVTVAGPIIGOIINLKASLDLLTAVTIETD--POTHOP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 V----ETTKKUTASFQTFLDKHSELINTINVSMLTETGERYKKVLSLFTEAIGKGYKASS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 LKCL-----KSLGLT------GELFEIRLTTSLFTNADVNTDIVKQLSDP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VAVLGECASDPTSISLSLLDKHSQIIN------K 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 ----LKASLDLLTA-----VTIETDPQTHQPVAVLGECASDPTSISL------ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 EGKYTADYLADKGVVPFLKVDKGLAEEQNGVQLMKP-----IDNLDSLLDFANERHI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIIN------- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 FGTKM-RSNILELNEQGIKD--VVEQQFEVAKQIJAKGLVPIJEPEVNINAKDKAEJEKV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Mismatches 73; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 EGLETVDNTL-KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN-TDI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 FLTSFFTTLESRITFLLRVTISPAAPTALKLISLNNIAKYINSIEKEVNIFTLV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 2; Length 1769;
Pred. No. 4.5;
                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 103.5; I
25.5%; Pred. No. 0.68
tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%;
19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

QY 83 IDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130 :	A:Experimental source: strain O157:H7, substrain RIMD 0509952 C:Genetics: A:Gene: ECs2776
OY 131 HQPVAVLGECASUPTS1SLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR1 188	Query Match 9.1%; Score 96.5; DB 2; Length 1345; Best Local Similarity 23.4%; Pred. No. 18; Matches 54; Conservative 36; Mismatches 70; Indels 71; Gaps 11;
697 YTGPLKVQQMKNFIDS	QY 50 LLNNVISKLI.PTNTDI-FGLKISNSLILDVKAE
D64000 D6400 0y 112 AVIITEDPOUPAVIGECRSDPYSTECANHYASTICANTINETHINETHINETHINETHINETHINETHINETHINE	
A;CLOSS=TELETRICES: GB:BAUGUOUT; FIDN:BABSSLYY.1; FID:913362244; GSPDB:GN00134	C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Jul-1999

```
C; Accession: B89944
R; Kuroda, M.: Ohta, T.: Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.: Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.: Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Oqasawara, N.: Hayashi, H.; Hiramatsu, R.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Molecule type: DNA
A;Residues: 1-825 <RUR>
A;Cross-references: GB:BA000018; PID:g13701417; PIDN:BAB42711.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A)Reference number: A89758: MUID:21311952; PMID:11418146 A)Accession: B89944 A)Accession: B89944 A)Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SA1447 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648 KLYSELYEELEKVRNMLLIQYDINQKQMKEIKLLKDELDRLKTVSAEILSKSREEVEERQ 707
                                                                                                                                                                                                                                              708 KKIFMLEEQIRTIAYSGQQPVKLLANQIN--IPTPRVNTDLSVKLINVKPSPSLTSKFFF 765
                                                                                                                                                                                                                                                                                                                76 -----LDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 129
                                                                                                                                                                                                                                                                                                                                                                           766 SLEFFDFQLETTPIMDAKQHNMDFTTVYDVLVSNLLIHYL-------- 806
                                                                                                                                                                                                                                                                                                                                                                                                                                             130 THOPVAVLGECASD-----PTSISLSLEDKHSQIINKFVNSVINTLKSTVSSLLQKEIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 NS------LILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 KASLDLLTAVTIETD----PQTHQPVAVLGECA-----SDPTSISLSLLDKHSQIINKF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 KAAL----LYTLEEECIKOGHTYLPINVVIDLTVDVLNYQDEEVIEPEKLDEMLQYLNEE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 VNSVINTLKSTVSSLLQKEICP---LIRIFIHSLDVNVIQQ-----VVDNPQ---- 206
                                                   1 KLEPVLHEGLETVDN-----TLKGILEKLK-VDLGVLQKSSAWQLAKQ 42
                                                                                                                                                                                   43 K------AQEAEKLLNNVISKLLPT---NTD----IFGLKISNSLI---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches 87; Indels 67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 DNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKL-LNNVISKLLPTNTDI-FGLKIS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal RNA processing protein RRPS - yeast (Saccharomyces cerevisiae)
N;Alternate names::protein YM9959.11c; protein YMR229c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 MAIYOFYLGDTLTILDRNPYQLIYDIK-----GIGFNKADQLARNIGIA---YNDNERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.5%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PLIRIFIHSLDVNVIQOVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               861 TL-----RYELEVSQPISDS 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 --HKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 ASQKEALOTAI 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SA1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Map position: 2
A.Introns: 35/2: 72/1: 119/2: 141/3: 183/2: 225/2: 325/2: 369/3: 492/2: 579/2: 645/3: 67
C;Accession: D64182
F;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, GGCayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                  A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Tille: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630 A;Accession: D64182
                                                                                                                                                                                                                                                                                                                                                                                         A)Cross-references: GB:U32789; GB:L42023; NID:q1574642; PIDN:AAC22753.1; PID:q1574651; C;Genetics:
G;Genetics:
A;Start codon: GTG
C;Superfamily: polydeoxyribonucleotide synthase (NAD+)
C;Superfamily: bolydeoxyribonucleotide synthase; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C09G5.8 - Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Date: 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19148; T20147
R;Palmer, S.
Submitted to the EMBL Data Library, November 1994
A;Reference number: 219080
A;Accession: T19148
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T1910 < WIL:
A;Residues: 1-1130 < WIL:
A;Cross-references: EMBL:246791; PIDN:CAA86762.1; GSPDB:GN00020; CESP:C09G5.8
A;Reference number: 219229
A;Reference number: 219229
A;Reference number: 219229
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gereica: 1-1130 < WIL:>
A;Cross-references: EMBL:246792; PIDN:CAA86767.1; GSPDB:GN00020; CESP:C09G5.8
A;Reperimental source: clone C52A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 IDGTVLKINDIALQNELGFISKAPRWAIAYKFPAQEELTLLNDVEFQVGRTGAITPVAKL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 EP--VFVAGVTVSNATLHNG----DEIERLNIAIGDTVVIRRAGDVIPQII----- 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 LTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 -- GVLHERRPDNAKPIIF-----PTNCPVC----DSQIIRIEGEAVARCTGGLFCAAQ 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VDNTLKGILE-KLKVDLGVLQKSSAWQLA-KQKAQEAEKLLNNV------ISKL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                                  A:Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.0%; Score 95; DB 2; Length 1130;
Best Local Similarity 24.9%; Pred, No. 19;
Matches 65; Conservative 33; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.0%; Score 95; DB 2; Length 679;
24.5%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 QKEICPLIRIFI--HSLDVN-----VIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 RKE---ALKHFVSRKAMDIDGVGGKLIEQLVD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Conservative
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-679 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:C09G5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
A Ancesalon: 327390
A Molecule type: DNA
A; Residues: 1-1729 <SKE>
A; Cross-references: BMBL: 249939; NID:9887599; PIDN:CAA90200.1; PID:9887610; MIPS:YMR229c
A; Experimental source: strain AB972
BMBO J: 15, 5701-574, 1996
A; Tille: RRP5 is required for formation of both 18S and 5.8S rkNa in yeast.
A; Reference number: S72446; MUID:97051828
A; Reference number: S72446; MUID:97051828
A; Reference number: S72446
A; Reduction: DNA
A; Residues: 1-1729 <VEN>
A; Reduction: DNA
A; Residues: 1-1729 <VEN>
A; Residues: I-1729 <VEN>
A; Residues: I-1729 <VEN>
A; Residues: RRP5 is required for pre-rkNa processing
C; Function: 13R
C; Function: required for pre-rkNa processing
C; Superfamily: ribosomal RNA processing
C; Keywords: nucleus; RNA binding
C:Species: Saccharomyces cerevisiae
C:Date: 19-0ct:1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S:7596; S7246
R:Skelton, J:; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.9%; Score 94.5; DB 2; Length 1729; Best Local Similarity 20.5%; Pred. No. 36; Matches 54; Conservative 44; Mismatches 87; Indels 79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 -----VTVAGPIIGQIINLKA----SLDL-------LTAVTIETD------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   805 SDKGLEVAFNGKFIGLVI.PSYAVDSRDIDJSKAFYINQSVTVYII.KTDDKNQKFILI.SLKA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 PQTHQPVAVIGEGASDPTSISLSLLDKHSQIINKEVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ETVDNTLKG------ILEKI.K------VDI.GVLQKSSAWQLAKQ--KAQE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 AEKLLNNVISKII.PTNTDIFGLKISNSLILDVKAEP1 --- DDGKGLNI,SFPVTAN --- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 6, 2002, 17:05:14 Job time: 916 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 IFIHS-LDV----NVIQQVVDNPQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              916 ANLHGRVDIAEVFDTYEETTDKKQ 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
```

```
August 6, 2002, 17:07:32 ; Search time 32.88 Seconds (without alignments) 253.184 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                   TREPVLHEGLETVDNTLKGI.........NVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                               105224
GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        105224 seqs, 38719550 residues
                                                                                                                                                                                                                     US-10-020-139-2_COPY_35_249
1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SwissProt_40:*
                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                      Sedneuce:
                                                                                                                                                  Run on:
```

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mus	P97361 mus musculu		Q07159 staphylococ	P42945 saccharomyc	Q9utk5 schizosacch	P89676 tomato mosa	P03587 tomato mosa		P43813 haemophilus	U	S	P36097 saccharomyc					simian	lister										Q92jh3 rickettsia		Z,		P71527 methanococc	
	ID		PSP_MOUSE	PLUN MOUSE	PLUN HUMAN	ALF STACA	YJK9 YEAST	ALM1_SCHPO	BRPO TOMK2	RRPO TOML	RRPO TOMS1	DNLJ HAEIN	YQ38_CAEEL	RRP5_YEAST	YKD3_YEAST	YGX7_YEAST	RRPO TOMK1	HAP1_HAEIN	TOXA_CLODI	VGLF_SV5	ISPG_LISMO	LBP_RAT	EG5_HUMAN	PMFF_PROMI	ISPG_CHLTR	GOG4_HUMAN	RLA0_METTL	PBPC_BACSU	Y55L_SYNY3	DDL_BUCAP	DGTP RICCN		ITAV_HUMAN	TBA3_DROME	NIFK_METMP	
	DB	1 1							۰,۰				7																							
	Length		235	278	256	500	1769	1727	16.16	1616	1616	679	1531	1729	1038	956	161	140	271(520	368	4	105,	138	.09	223	33	99	26	30	C	35	104	45	462	
æ	Query Match		7	_		0.01	0.01	o a	7 0	, m	. m		0.6	0.00	000	60	0	. 6	9.	, c	0 00	- d										0				
	Score		44) _								9	์	. ~	500	10	ıٽ	γģ	100	0 00	ο σ σ	o o	0 00	87.5		V.	0 00	•	ហ	ìц	2.00		~	83.5	
	Result No.		-	• (4 0	n •	gr Li	7 4	9 1	~ 0	oo	, ,) r-	101	7 -	γ. Γ	- u	1 -	7.7	À (0 0	90	3 -	100	2 6	200	1 C	9 (4	200	4 C	000	30%) r	30	3 E	

010339 schizosacch P33420 saccharomyc P46674 saccharomyc P40108 cladosporiu P70782 agrobacteri P16228 salmonella P54861 saccharomyc Q9h583 homo sapien Q58438 methanococc O07585 bacillus su P30436 oncorhynou				brata; Euteleostomi; Huridae; Murinae; Mus.		armark K., otein and salivary	IN IN THE PAROTID GLAND. PRODUCTION IS COORDINATED	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way on modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	RY PROTEIN. EF3 CRC64;	B 1; Length 235; 17; 74; Indels 13; Gaps 4;
615 1 YBMZ_SCHPO 868 1 N180_YEAST 1301 1 SAC3_YEAST 466 1 DIML_CLAHE 699 1 EFG AGRTU 466 1 FLID_SALTY 757 1 DIML_YEAST 2144 1 BP28_HUMAN 366 1 YA32_METJA 444 1 TBA_ONCKE 446 1 TBA3_MOUSE	ALIGNMENTS	PRT;	Us, Last sequence upware) 35, Last annotation update) protein precursor (PSP).). Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae	SEQUENCE FROM N.A. TISSUE-Parotid gland; MEDLINE-8521456; PubMed=2582349; Madsen H.O., Hjorth J.P.; "Modecular cloning of mouse PSP mRNA."; Nucleic Acids Res. 13:1-13(1985).	SEQUENCE OF 1-87 FROM N.A. STRAIN=C3H; TISSUE=Spleen; MEDLINE-87004556; PubMed=2428613; POULSEN K., Jakobsen B.K., Mikkelsen B.M., Harmark K., Nielsen J.T., Hjorth J.P.; "Coordination of murine parotid secretory protein and sali	1986). S THE MOST ABUNDANT PROTEI NOT KNOWN; HOWEVER, ITS F LIVARY AMYLASE.	ry is copyright. It is pro Institute of Bioinformatic ormatics Institute. There institutions as long as tatement is not removed. Ilicense agreement (See ht	CAA25846.1; AAA40009.1; OMAA40009.1; OMS. PSP. Signal. POTENTIAL. 1 235 PAROTID SECRETORY F. AA; 24753 MW; 23311BAELEGEEEFFY	27.8%; Score 294.5; DB 32.7%; Pred. No. 6.5e-17
20238888867777		STANI	(Rel. UR (Rel. 3)	Metazoa; Metazoa; Sutheria;	COM N.A. Otid glan 215456; P 1, Hjorth cloning ids Res.	F 1-87 FR ; T1SSUE= 004556; P ; Jakobse T., Hjort	pression. 1891-1896 ON: PSP 1 NCTION IS	- PROT ent he Swiss an Bioint on-profit nd this s equires a	97; CAA24 07; AAA44 06; AAA4 11; SQMS. 17787; Psi 17787; Psi and; Sig	. Match Local Similarity Les 69; Conserva
83.5 83.5 83.5 83.5 83.5 82.5 82.5 82.5 81.5		SP_MOUSE D PSP_MOUSE STANDARD; D D7743; T 01-AUG-1988 (Rel. 08, Created	1-AUG-1988 11-NOV-1997 arotid sec	fus musculu Sukaryota; Ammalia; E	SEQUENCE FE SEQUENCE PARK REDLINE-855 Andsen H.O. Molecular	SEQUENCE OF STRAIN=C3H MEDLINE=87 Poulsen K. Nielsen J.	amylase ex EMBO J. 5: -!- FUNCTI ITS FU WITH T	This SWISS between the Europe to the by no modified a entities r or send an	EMBL; X016 EMBL; M268 EMBL; M268 EMBL; M268 EMBL; M268 PR; A2303 MGD; MGI:9 Parotid 91 SIGNAL CHAIN	Query Match Best Local Si Matches 69;
		RESULT PSP_MO ID P AC P DT 0		S C C C C C	RR RX RY	R R R R R R R R R R R R R R R R R R R	F 7 0 0 0	000000000000000000000000000000000000000	SOTTER	Que Bes Mat

SUMMARIES

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERMINESPOND FUNDED-Palate;
MEDINES-9240770; Pubmed-10224143;
MEDINES-9240770; Pubmed-10224143;
MESTON W.M., Leclair E.B., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Mal L., Tuan R.S., Greene R.M.;
"Differential display identification of plunc, a movel gene expressed in embryonic palate, nasal epithelium, and adult lung.";
in embryonic palate, nasal epithelium, and adult. Lung.";
                                                                                                                                                                    114 ASLDLLTAVTIETOPQTHQPVAVLGECASDPTSISLSLLDKHSQ11NKFVNSVINTLKST 173
                                                                                                                                                                                                56 SKLLPTNTDIFG--LKISNSLILDVKAEPLDDGKGLNLSFPVTANVTVAGPIIGQIINLK 113
                                                                                                                         75 LGNLKSFTSLNGLLLKINNLKVLUFQAKLSSNGNGIDLITVPLAGFASLVLPFIGKTVDIS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeClair E.E., Nguyen L., Bingle L., MacGowan A., Singleton V., Ward S.J., Bingle C.D.:
"Genomic organization of the mouse plunc gene and expression in the developing alrways and thymus.";
3 EPVLHEGLETVDNTLK-----GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI 55
                                         19 ESLLGE-LGSAVNNLKII.NPPSEAVPQNLNLDVELLGGATSWPLAKNSILET---LNTAD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weston W.M., LeClair E.E., Trzyna W., McHugh K.M., Nugent P.,
Lafferty C.M., Ma L., Tuan R.S., Greene R.M.;
J. Blol. Chem. 275:8262-8262(2000).
J. Blol. Chem. 275:8262-8262(2000).
I. FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor progression (By similarity).
-:- SUBCELLULAR LOCATION: Secreted (By similarity).
-:- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 11, Last ammotation update)
Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 284:792-797(2001).
                                                                                                                                                                                                                                                                                                                                                                                                             278 AA.
                                                                                                                                                                                                                                                             174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                    195 LSTVLONFLCPLLQYVLSTLNPSVLQGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21290678; PubMed~11396972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF356785; AAK63069.1; -.
EMJL; U69172; AAB63256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1338036; Plunc.
Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Sv
                                                                                                                                                                                                                                                                                                                                                                                                                PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein).
                                                                                                                                                                                                                                                                                                                                                                                                PLUN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                  á
                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                    ŏ
                                                                                                δ
```

```
85 DGKGLNLSFPVTANVTVAGP11GQ11NLKASLDLLTAVT1ETDPQ--THQPVAVLGECAS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 DGHRLYVTIPLGLTLNVNMPVVGSLLQLAVKLNITAEVLAVKDNQGRIH----LVLGDCTH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 SPGSLKISLLNGVTP-VQSFVDNLTGILTKYLPELIQGKVCPLVNGILSGLDVTLVHNIA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein) (Lung specific X protein) (Nasopharyngeal carcinoma-related protein) (Tracheal epithelium enriched protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 LGILENIPLLDVIKSGGGNSNGI,VGGLLGKLTSSVPLLNNILDIKITDPQLLELGLVQSP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 IGVLQKSSAWQLAKQKAQEAEKILANVISKL---LPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwao K., Watanabe T., Fujiwara Y., Takami K., Kodama K.,
Higashiyama M., Yokouchi H., Ozaki K., Monden M., Tanigami A.;
"Isolation of a novel human lung-specific gene, LUNX, a potential
molecular marker for detection of micrometastasis in non-small-cell
                                                      4 X 6 AA REPEATS OF G-[LPQ]-[PL]-L-P-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of the human plunc gene, a gene product with an upper airways aind nasopharyngeal restricted expression pattern."; Biochim. Biophys. Acta 1493:363-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLUNAN STANDARD; PRT; 256 AA.

Q9NP55; Q9NZTO;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

Protein Plunc precursor (Palate lung and nasal epithelium clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Z.W., Yao K.T., Xu L.G., Ken C.P., Lan K., Xie L., Zhang L., Liu W.D., Zhow W., Wang L.;
"Cloning a new gene related to nasopharyngeal carcinoma.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
7F40BED9859188FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelec
Mammalia: Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 185.5; DB 25.0%; Pred. No. 5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 5e-0
44; Mismatches
                               PROTEIN PLUNC
POTENTIAL.
                                                                                                                                            REPEAT 2.
                                                                                                                                                                               REPEAT 3
                                                                                                                                                                                                                      REPEAT 4
                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20472055; Pubmed=11018263;
Bingle C.D., Bingle L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21150203; PubMed=11251963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Cancer 91:433-437(2001).
                                                                                                                                                                                                                                                                                                                           28611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 ELLIHGLQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                   SECUENCE
                                                                          DOMAIN
                                                                                                                                                    REPEAT
       SIGNAL
                                                                                                             REPEAT
                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOOR SERVICE REPAYED BY THE SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
```

```
RA Deloukas P., Matthew's L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Beridgeman A.M., Brown A.J.,
RA Clappan J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clappan J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clappan D.V., Collier R.E., Connor R., Corby N.R.,
RA Lington A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Krights A., Laird G.K., Lawlor S.,
RA Minckle E., Mistry D., McConnachle L.J., McLay D.M., Johnson D.,
RA Mines V., Martin S.L., McConnachle L.J., McLay W., McLay K., McMurray A.A.,
RA Mines S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,
RA Hillinge L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Mining L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Roders J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWB. outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21317946; PubMed-11425234;
Lindahl M., Stahlbom B., Tagasson C.;
Lindahl M., Stahlbom B., Tagasson C.;
"Identification of a new potential airway irritation marker, palate
lung nasal epithelial clone protein, in human nasal lavage fluid with
two-dimensional electrophoresis and matrix-assisted laser
description/ionization-time of flight.";
Electrophoresis 22:1795-1800(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Upper airways and masopharyngeal regions, including trachea and masal epithelium. Expressed in lung cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: May be involved in the airway inflammatory response after exposure to irritants. May be associated with tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN PLUNC.
Q -> K (IN REF. 1; AAF70860).
EDF152FBC35315BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 95-152; 157-167 AND 214-232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and some other types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBČELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF214562; AAG13653.1; -. EMBL; AF172993; AAF70860.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB024937, BAA93633.1;
EMBL, AF158425.1;
EMBL, AL121901; CAC03549.1;
EMBL, BC012549; AAH12549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 256 E 220 C 256 A 256 A 25712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rogers
```

Gaps

: 9

16.8%; Score 178; DB 1; Length 256; 24.5%; Pred. No. 1.8e-07; Live 44; Mismatches 92; Indels

Conservative

Best Local Similarity Matches 46; Conserv

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                       184 PGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPELVQGNVCPLVNEVLRGLDITLVHDIV 243
                                   65 LGILENLPLLDIIJKPGGGTSGGLIGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP 124
                                                                         85 DCKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                               01-0c1-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase).
28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Witke C., Goetz F.; and characterization of the gene encoding the cloning, sequencing, and characterization of the gene encoding the class I fructose-1,6-bisphosphate aldolase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILKE C., GOELZ F.;
J. Bacteriol. 1755-7499(1993).
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate - glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
-!- SINILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHIFF-BASE WITH DIHYDROXYACETONE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; $33358; $33358.

PIR; $4943; $4943.

PIR; $49423; $1A52

InterPro; IPR000741; Aldolase_I.

Pfam; PF00274; glycoltti_endzy; 1.

Propon: P001128; Aldolase_I: 1.

PROSITE; PS00158; Aldolase_CLASS_I; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol, 175:7495-7499(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDI,INE=94042930; PubMed=8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94042930; PubMed-8226699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase, Schiff base, Glycolysis.
INIT_MET 0 0 0
BINDING 211 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X71729; CAA50663.1; -.
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus carnosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kula M.R., Brockamp H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                               203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                     244 NMLIHGLQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID~1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TM300
                                                                                                                                                                                                                                                                                                                                                               ALF_STACA
007159:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carnosus.
                                                                                                                                                                                                                                                                                                                                             ALF_STACA
                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                   ò
                                                                                 ò
                                                                                                                 a
                                                                                                                                                       ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 V----ETTKKDTASFOTFLDKHSELINTINVSMLTETGERYKKVLSLFTEAIGKGYKASS 510
362 KLNIILSLLKK-----IRLERYEVRLIITDLIYLSEILEDKSQLVELFEYFISINEDLV 415
                                   76 I.DVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETD--PQTHQP 133
                                                                    416 LKCL-----KSLGLT-----GELFEIRLTTSLFTNADVNTDIVKQLSDP 454
                                                                                                     134 VAVLGECASDPTSISLSLLDKHSQIIN-----K 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jimenez M., Petit T., Gancedo C., Goday C.;
"The alm!+ gene from Schizosaccharomyces pombe encodes a coiled-coil
protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                          162 FVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLOTLI 215
                                                                                                                                                                                              "Generation and analysis of GFP-gene fusion library of fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                               ALM1_SCHPO STANDARD; PHT: 1727 AA 09UTK5; 01313; 09UTR8; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Abnormal long morphology protein 1 (Sp8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL133357; CAB62414.1; -.
EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
463
740
1106
1427
1555
                                                                                                                                                                                                                                                                                                                                                                                                      ALM1 OR SPACI486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443
542
804
1223
1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOKINESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-968 H90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ding D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeast."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                ALM1_SCHPO
                                                                                                                                                                                                                                                                                                                   q
                                                                                                         ò
                                                                                                                                         qq
                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                          ..
J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
ω
                                                                                                                                                         93 KGIVPFLKVDKGLAEEADGVQLMK-P1PDLDKLLDRA----NERGIFGTKM-RSNILE 144
                                                                                                                                                                                              145 NNKEAIE--KVVKQQFEVAKEIIAAGLVPIIEPEVNINAKDKEAIEANLAEAIKAELDNL 202
                                                                                                                                                                                                                                                                 118 -----LLTAVTIET------DPQTHQPVAVLGECASDPTSISLSLDKHSQIINKF 162
                                                                                                                                                                                                                                                                                               203 KKDQYVMLKLTIPTKVNAYSELIEHPQVIRVVALSGGYSRDEAN---KILKQNDGLIASF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLI 75
                                                                                          48; Gabs
                                                                                                                          18 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLI,NNVISKLLPTNTD1FGI,KISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
200.0 kDa protein in GZF3-IME2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 106; DB 1; Length 1769; 19.2%; Pred. No. 1.4;
                                                   10.0%; Score 106; DB 1; Length 295; 25.9%; Pred. No. 0.14; tive 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      064480DlD249B241 CRC64;
       295 AA; 32720 MW; A189E75574F1FCC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>::</del> ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Mismatches
                                                                                          Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288C / FY1679;
MEDLINE=96090136; PubMed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0003645; YJL109C.
InterPro; IPR000357; HEAT_repeat.
PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1769 AA; 200080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X85021; CAA59385.1; -. EMBL; Z49384; CAA89404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1767
                                                                                                                                                                                                                                                                                                                                    163 VNSVINTLKSTVS 175
                                                                                                                                                                                                                                                                                                                                                                     260 SRALVSDLNAQQS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein
REPEAT 1729 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                          Best Local Similarity
Matches 50; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical 200.
YJL109C OR J0808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --
--
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        YJK9_YEAST
P42945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
         SEQUENCE
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          YJK9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                               g
                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                     qq
```

S

Š

qq

ò

QQ

g ó

ó

```
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          RRPO_TOML
                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                      ò
                                                                             ò
                                                                                                                                                              δ
                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRPO_TOMK2 STANDARD, PRT; 1616 AA.
P89676; P90349;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                      78 VKAEPIDDGKGLNLSF-PVTANVTVAGPIIGQ/INLKASLDLLTAVTIETDPQTHQPVAV 136
                                                                                                                                                                                                                                                            459 VQAELLSTKMRQEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSRNVPATVQ--VA 516
                                                                                                                                                                                                                                                                                                   137 LGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSL--D 194
                                                                                                                                                                                                                                                                                                                                           517 LDEYAQNPSTASETLVNK--ELAN-----FSSIKEAVSKTLE-----LREKVRALECD 562
                                                                                                                                                                             404 KLQLDRLTNKFSSFCEQVKQRIPVVKQQRSEIVRNNIYMNFLSES-----LETSNNNLTK 458
                                                                                                                                         23 KLKVDLGVLQKSSAWQLAKQ-----KAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Biol. (Mosk) 31:826-830(1997).
FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)].
Tomato mosaic virus (strain Kazakh K2) (ToMV) (TMV strain K2).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANDOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belenovich E.V., Generozov E.V., Novikov V.K., Zavriev S.K., "Properties and structure of the tobacco mosaic virus strain K2 \,
                                                     9.4%; Score 99.5; DB 1; Length 1727; 26.1%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-DIRECTED RNA POLYMERASE.
                                                                                                  74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
W; C2F5CE0C8C965336 CRC64;
197858 MW; F820BF8D9C132644 CRC64;
                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interpro: IPR000606; Viral_helicasel.
Pfam; PF00978; RNA_dep_RNApol2; 1.
Pfam; PP01443; Viral_helicasel. 1.
Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001788; RNA_dep_RNApol2.
Interpro; IPR002588; V_methyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98012318; PubMed-9454068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          833 840 ATE
                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 292909; CAB07439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z92909; CAB07438.1;
                                                                                                      49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1116
840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA REPLICATION.
    1727 AA;
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                    195 VNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=138312
                                                                                                                                                                                                                                                                                                                                                                                                                             563 VEIQKOTV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
NP_BIND
SEQUENCE
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
RRPO_TOMK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                        Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_TOML STANDARD; PRT; 1616 AA.
P03567; 041352;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation 
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13) HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSRDV 639
                                                                                                                                                                                                                                                                                                                                                536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                    79; Indels 33; Gaps
                                                                                                                                                                                                                                  23 KLKVDLGVLQKSSAMQLAKQKAQEAHKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPING AND AN RNA HELICASE. MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the tobacco mosaic virus (tomato strain) genome and comparison with the common strain genome."; J. Biochem. 96:1915-1923(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1616 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., Aoyagi M., Yamanashi Y., Saito H., Ikawa S., Meshi T.,
      .DB 1; Length 1616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHYLTRANSFERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
W; A8EC8929B5CF7CAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HETWEEN COLONS FOR GLN-1116 AND GLN-1118.
                                                             ; Pred. No. 4.9;
44; Mismatches
9.3%; Score 98.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001788; RNA_dep_RNApol2.
InterPro: IPR002588; V_methyltransf.
InterPro: IPR000606; Viral_helicasel.
Pran: PP00978; RNA_dep_RNApol2; 1.
Pfam: PP01443; Viral_helicasel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-85157522; PubMed-6549393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01660; Vmethyltransf; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X02144; CAA26085.1; -. EMBL; X02144; CAA26082.1; -.
                                                                   20.4%;
                                                                                                                    40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833 84
1616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A04195; WMTM8T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA REPLICATION
                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=12252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okada Y.;
                  Query Match
```

Score 98.5; DB 1; Length 1616;

9.38;

Query Match

```
This SWISS-PROT cutry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09YXD6: 09MJ37;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (183 kDa protein) (Contains: Methyltransferase/RNA helicase (MT/HEL) (126 kDa protein)).
Tomato mosaic virus (strain S-1) (TOWY).
Viruses; SSRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICOSE.
-1- MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                          589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSKDV 639
                                                                                                  536 KMSVDMPVLD------IRKKMEETEEMYNALSELSVLKNSDKFDVDVFSOMCOSLEVDP 588
                                                                                                                                              83 IDDGK------GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                              131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIKI 188
                                                                                                                                                                                                                                                                        640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHMATASSLIHKQMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL RNA REPLICATION.
                  33; Gaps
                                                         23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou x., Xue C., Chen Q., Qi Y., Li D.; "Complete nucleotide sequence of a Chinese isolate of tomato mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-DIRECTED RNA POLYMERASE.
METHYLTRANSFERASE/RNA HELICASE.
                  79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
W: SDBBFB2FADCC5C0C CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1616 AA.
                      Mismatches
20.4%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001788; RNA dep_RNApol2.
Interpro; IPR002588; V_methyltransf.
Interpro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00978; RNA_dep_RNApol2; 1. Pfam; PF01443; Viral_helicasel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183542 MW;
                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ132845; CAB36997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01660; Vmethyltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ132845; CAB36998.1
                                                                                                                                                                                                                                                                                                                        189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                               697 YTGPLKVQQMKNFIDS 712
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833 8,
1616 AA;
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID=138314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRPO_TOMS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRPO_TOMS1
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                       õ
                                                                                                                                                                                              g
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                            δ
```

23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82

9.3%; Score 98.5; DB 1; Length 1616;

Pred. No. 4.9;

20.4%;

Query Match Best Local Similarity

Mismatches

44;

Conservative

40;

Matches

δ

Indels

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 EEP-SIKGSMARGELQLAGLSGDVPESSYTRSEEIESLEQFHWATASSLIHKQMCSI--V 696
: | : | : | : | 589 MTAAKVIVAVMSNESGLTLTFEQPTEANVALA------LQDSEKASDGALVVTSRDV 639
                                                      83 1DDGK------GLNI,SF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                              131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLJRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDELINE-95350630; PubMed-7542800; Piblicon R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Witterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
LIGN OR LIG OR HI1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (deoxyribonucleotide)(M) = AMP + nicotinamide nucleotide +
(deoxyribonucleotide)(N+M).
-! SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY.
-! SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR004150; DNA_ligase_OB. IPR004149; DNA_ligase_ZBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001679; DNA_ligase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32789; AAC22753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000445; HHH.
IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001357; BRCT
                                                                                                                                                                                                            189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                              697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O87703; 1B04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGR: HI1100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                                        DNLJ_HAEIN
P43813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                          DNLJ_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                              õ
```

```
RRP5_YEAST
Q05022;
                                                                                            SEQUENCE
                                                                                                                                     Query Match
                                                                   DOMAIN
                                                    DOMAIN
                                                                               DOMAIN
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRP5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                             294 IDGTVLKINDIALQNELGFISKAPRWAIAYKFPAQEELTLLNDVEFQVGRTGAITPVAKL 353
                                                                                                                                                                                                                                                                                                                                                           59 LPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDL 118
                                                                                                                                                                                                                                                                                                                                                                                    354 EP--VFVAGVTVSNATLHNG----DEIERLNIAIGDTVVIRRAGDVIPQII----- 398
                                                                                                                                                                                                                                                                                                                                                                                                                119 LTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                          399 --GVLHERRPDNAKPIIF-----PTNCPVC----DSQIIRIEGEAVARCTGGLFCAAQ 445
                                                                                                                                                                                                                                                                          52; Gaps
                                                                                                                                                                                                                                                                                                      13 VDNTLKGILE-KLKVDLGVLQKSSAWQLA-KQKAQEAEKLLNNV------1SKL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                  SMART; SM00532; LIGANC; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS01055; DNA_LIGASE_N1; 1.
Ligase; DNA replication; NaD; Complete proteome.
DOMAIN 601 679 BRCT.
                                                                                                                                                                                                                                         / Match 9.0%; Score 95; DB 1; Length 679; Local Similarity 24.5%; Pred. No. 3.1:
                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQ38_CAEEL STANDARD; PRT; 1531 AA. 009459; 009513; 0.-NOV-1997 (Rel. 35, Created) 61-NOV-1997 (Rel. 41, Last sequence update) 61-MAR-2002 (Rel. 41, Last annotation update) 61-MAR-2001 (Rel. 41, Last annotation update) 61-Mypothetical 174.9 kDa protein CU9G5.8 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmer S., Sulston J.; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                          AMP (BY SIMILARITY).
4C0C23E25D70FF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO C.ELEGANS 2K666.1 AND 2K666.4.
                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 QKEICPLIRIFI--HSLDVN-----VIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                   ProDom; PD003944; DNA_ligase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z46791; CAA86762.2; -.
EMBL; Z46792; CAA86762.2; JOINED.
 Pfam; PF00533; BKCT; 1.
Pfam; PF01653; DNA_11gase_N; 1.
Pfam; PF03120; DNA_11gase_OB; 1.
Pfam; PF03119; DNA_1igase_ZBD: 1.
Pfam; PF00633; HHH; HH; 1.
                                                                                                                                                                                             125 125 A
679 AA; 75188 MW;
                                                                                                                                                                                                                                                                             52; Conservative
                                                                                  SMART; SM00292; BRCT; 1
SMART; SM00278; HhH1; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS.
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
     DR
DR
DR
DR
DR
DR
DR
DR
SO
                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288C / AB972;
Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venema J., Tollervey D.; "RRP5 is required for formation of both 18S and 5.8S rRNA in yeast."; EMBO J. 15:5701-5714(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 -----LDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   766 SLEFFDFQLETTPIMDAKQHNMDFTTVYDVLVSNLLIHYL-----------------0 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 THQPVAVLGECASD-----PTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEIC 183
                                                                                                                                                                                                                                                                                                                                          Match
Local Similarity 24.9%; Pred. No. 8.7;
es. 65; Conservative 33; Mismatches 73; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLEPVLHEGLETVDN------TLKGILEKLK-VDLGVLQKSSAWQLAKO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 K------IFGLKISNSLI---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 15:5701-5714(1996).

-:- FUNCTION: INVOLVED IN THE BIOGENESIS OF RRNA. REQUIRED FOR THE FORMATION OF 188 AND 5.88 RRNA.

-:- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

-:- SIMILARITY: CONTAINS 4 HAT REPEATS.

-:- SIMILARITY: CONTAINS 1 1 S1 MOTIF DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                       1150 1154 POLY-ASP.
1531 AA; 174862 MW: A453990AFODEBC2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rRNA biogenesis protein RRP5.
RRP5 OR FM11 OR YMR229C OR YM9959.11C.
                                                                                                                                      POLY-SER.
POLY-ASN.
POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE=97051828; Pubmed=8896463;
EMBL, 246792; CAA86767.2; The Embler of CAA86767.2; JOINED. WormPep; CO965.8; CE25774. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 PLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861 TL-----RYEIEVSQPISDS 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
```

```
MEDLINE-94262309; PubMed-8203146; MEDLINE-94262309; PubMed-8203146; Purnelle B., Skala J., van Dyck L., Goffeau A.; Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene and four new open reading frames including a leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               865 PKVKEEKKKVESNIEDPVDSSIKSWDDLS-----IGSIV---KAKIKSVKKNOLNVILA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                       687 DTIENIVPGRTIITVHVIEKTKDSVIVEIPDVGLRGVIYVGHLSDSRIEONRAOLKKLRI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 -----VTVAGPIIGQIINLKA----SLDL------LTAVTIETD------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQTHQPVAVLGECASDPTSISLSLLDKHSQ11NKFVNSVINTLKSTVSSLLQKE1CPLJR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747 GTELTGLVIDK--DTRTRVFNMSLKSSLIKDAKKETLPL1YDDVKDLNKDVPMHAYIKSI 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             805 SDKGLFVAFNGKFIGLVLPSYAVDSRDIDISKAFYINQSVTVYLLRTDDKNQKFLLSLKA 864
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                11 ETVDNTLKG-----ILEKLK-----VDLGVLOKSSAWQLAKQ--KAQE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 AEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPI----DDGKGLNLSFPVTAN---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                         16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00N-1994 (Rel. 29, Created)
01-00N-1994 (Rel. 29, Last sequence update)
01-0NN-1994 (Rel. 29, Last annotation update)
Hypothetical 118:9 kDa protein in PTMI-IXR1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                             8.9%; Score 94.5; DB 1; Length 1729; 20.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                          39BF46E5587B3B0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1038 AA
                                                                                                                               SI MOTIF 1.
SI MOTIF 2.
SI MOTIF 3.
SI MOTIF 4.
SI MOTIF 6.
SI MOTIF 6.
SI MOTIF 7.
SI MOTIF 9.
SI MOTIF 9.
SI MOTIF 11.
HAT 1.
                                                                                                                     Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 IFIHS-LDV----NVIQQVVDNPQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 ANLHGRVDIAEVFDTYEE1TDKKO 939
                                                                                                      PROSITE; PS50126; S1; 11.
Nuclear protein; rkNA processing;
                                                                                                                                                                                                                                                                                      HAT
                                                                                                                                                                                                                                                                                                      HAT
                                                                                                                                                                                                                                                                                                                             193133 MW;
                                                                                                                                                                                                                                                                                                                                                                                            44
EMBL; Z49939; CAA90200.1; -. HSSP; P05055; 15RO.
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                        InterPro; IPR003107; HAT.
InterPro; IPR003029; Sl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                             1336
1487
1594
                                                                                                                                                                                                                         1083
1159
                                                                                                                                                                                                                                                 1245
                                                                               SMART; SM00386; HAT; 2.
                                                                                          SMART; SM00316; S1; 12.
                                                                                                                                  200
                                                                                                                                                         580
676
769
863
971
                                                                                                                                                                                                                                                                                                    1664
1701
                                                                                                                                                                                                                                                                                                                                AA:
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 54; Conserv
                           SGD; S0004842; RRP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKLO33W OR YKL246.
                                                                     ; S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                               1265
1455
1561
1666
1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                  Pfam; PF00575,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKD3_YEAST
P36097;
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                   DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                              DOMAIN
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                     DOMA I N
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKD3_YEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \dot{}
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 VKAEPIDDGKGLN---LSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 AVLGECASDPTS1SL----SLLDKHSQIINK----FV-----NSVINTLKSTVSSL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05 SWL-TATSGUINIALEAFIPKLLKKNNESIDEALATFVSILLTRCENSLNNCEKVLVSTL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 VLHQFFKSVRSQRYHKEFFSNSKPNLLPALGHSVTILLKILEQSPQNNELQFKALASLEV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 IKVNKLTDIRELSDTKLKHEINQSFMFNGPI--------VLLRTDGKTHRDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VLHEGLETV-------DNTLKGILEKLKVDLGVLQKSSAWQLAKQKA-QEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LKISNSLI-----LD 77
protein and a homologue to the yeast mitochondrial regulator ABE2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-OST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8%; Score 93.5; DB 1; Length 1038;
1.4%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            D068AEC2F4556A72 CRC64;
                                                                                              (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             958 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 LOKEICPLIRIFIHSEDVNVIQQVVDNPQHK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 VHLEKDPMSKLPSHLVK---LKEVVNEDLHK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 LLNNVISK-----LLPTNTDIFG------
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
                                                                                                                                                                                                                                                                                               EMBL; X71622; -; NOT_ANNOTATED_CDS.
EMBL; 228033; CAA81868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kramer B., Kramer W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                           594 610 POT
869 885 POT
1038 AA; 118888 MW;
                                                             SEQUENCE OF 913-1038 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 21.4 Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                      PIR; S37854; S37854.
SGD; S0001516; YKL033W.
                                                                                                                                                                                                                                                                                                                                                             SGD; Suverier, Hypothetical protein; T
                         reast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGX7_YEAST
P53076:
                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                    Rieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGX7_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
```

```
Job time: 876 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
           DR DR DR PET FET SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPO_TOMK1 STANDARD; PRT; 1616 AA.
090178; 090177;
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 LNLS----PPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 YLINKGQISKCINYIDNEIPDLLKNNLELVFELKLANYLVMIKKSSSKDDDEIENLILKG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       838 QELSNEFIYDTKIPQSLRDRFSGQLSNVSALL-----AYSNPLVEAPKEISGYLSDEY 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Tobacco Mosaic virus.";
Mol. Biol. (Mosk) 34:172-176(2000).
-i. FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 LIHEGLVDV---AKGFLKDLQKDAVNVNGQHSESKDVIRHNER-QIMKEERMVKIRQELR 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              properties and genome structure of the Kazakh isolate Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VLHEGLETVDNTLKGILEKIKVDL------GVLQKSSAWQLAKQK----AQEAE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 KLLN------NVISKLLPTNTD-IFGLKISNSLILDVKAEPIDDG-----KG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANDOUS: READDHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLN-1116 AND GLN-1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 8.7%; Score 92.5; DB 1; Length 958; Best Local_Similarity 22.8%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
; 335ADD152949F8C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            891 LQERLFQVSNNTILTFLHKDSECA---LENVISNTRAMLSTLLE 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 -----PTSISLELDKHSQIINKFVNSVINTLKSTVSSLLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196905; PubMed*10732356; Belenovich E.V., Novikov V.K., Zavriev S.K.; "Biological properties and genome structure o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPPING AND AN RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                  IPR003878; SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 AA; 108178 MW;
                                                                                                                                                                                                                          EMBL; 272749; CAA96943.1; -.
                                                                                                                                                                                                                                                                   SGD; S0003196; VID30.
InterPro; IPR003877; SPRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00622; SPRY; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=138311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRPO_TOMK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

q

```
131 HQPVAVLGECASDPTSIS--LSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 EEP-SIRGSMARGELQLAGLSGDVPESSYTRSEE1ESLEGFHMATASSLIHKOMCSI--V 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 KMSVDMPVLD-----IRKKMEETEEMYNALSELSVLKTSDKFDVDVFSQMCQSLEVDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 IDDGK-----GLNLSF--PVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 33; Gaps
                                                                                                              InterPro; irroucev.

Pfam; PF00978; RNA_dep_RNApol2: 1.

Pfam; PF001443; Vira_helicasel: 1.

Pfam; PF00560; Vmethyltransf: 1.

Pransferase; RNA-directed RNA polymerase; Helicase: ATP-binding.

(HAIN 1116 METHYLTRANSERASE/RNA HELICASE.
                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 19.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                   ATP (POTENTIAL). W; 4BF9913CE791DE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     80;
                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 6, 2002, 17:07:34
                                              InterPro; IPR001788; RNA dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR004606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                            1616 AA; 183606 MW;
EMBL; AJ243571; CAB62911.1; -. EMBL; AJ243571; CAB62912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 FIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 YTGPLKVQQMKNFIDS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                        833
                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                        NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

```
August 6, 2002, 17:09:28; Search time 111.35 Seconds (without alignments) 334.027 Million cell updates/sec
                                                                                                                                                                                             1 KLEPVLHEGLETVDNTLKGI.....NVIQQVVDNPQHKTQLQTL1 215
                                                                                                                                                                                                                                                                                                          562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           562222 segs, 172994929 residues
                                                                                                                                                            US-10-020-139-2_COPY_35_249
                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_fungi:*
sp_human:*
                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                Searched:
                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	4405	Ugdept mus musculu 094794 mus musculu 09643 mus musculu 096460 mus musculu 096146 homo sapien 061114 mus musculu 099913 staphylococ 099731 staphylococ
SUMMARIES	Q9BQQQ Q96DR5 P79124 P79125 Q9D734 Q63471	090592 090794 0900x3 0906P0 0909HK6 061114 0999JB
DB	44991111	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
% Query Match Length DB	00000000000000000000000000000000000000	22222222222222222222222222222222222222
% Query Match	100.0 99.2 31.4 30.5 27.8 24.8 14.6	14.0 114.0 113.7 112.2 110.8
Score	1061 1053 333.5 324 294.5 154.5	148.5 148.5 148.5 145.5 129 126 115
Result No.	1784897	1111099110991109

0991t0 tomato mosa 059040 methanococc 094mnfs tobacco mos 09ja03 tobacco mos 09ja04 tobacco mos	099tn0 staphylococ 0911r8 tomato mosa 0911r9 tomato mosa 061769 mus musculu 09dut4 porcine rub	Q49540 mycoplasma Q92cg8 listeria in Q9xtu2 caenorhabdi P94750 escherichia	09d749 mus musculu 09erv5 mus musculu 005701 rattus ratt 09k899 vibrio chol 07511 caenorhabdi 09k847 vibrio chol 09h871 drosophila	09fvx8 oryza sativ 09fvx8 oryza sativ 09kp22 vibrio chol 0599f6 streptococc 09b3y0 plasmodium 09n218 caenorhabdi 09yza2 simian para
2 0991T0 7 059040 2 09WNG5 2 09JA03	16 099TN0 12 099TR8 12 0991R8 11 061769 12 090FT4	049548 6 092CG8 09xTU2 P94750 6 P76347		10 09FVX8 10 09FVX8 16 09KP32 2 059986 5 09BJY0 5 09YZA2
1116 1 211 1 866 1 1116 1			52333	
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	ကေတာ့ ထား ထား ထား ကေတာ့ တာ တာ ထား ထား) & & & & & & & & & & & & & & & & & & &	00000000000000000000000000000000000000	သတ္တတ္ထတ္ထ ပလုလ်လုလ်လုပ်
98 97 .5 97 .5 97 .5	0 40 0 40 0 4 40 0 3 . 50 0 6 6 6	92 92 98 98 98 98	91.5 91.5 91.5 91.5 91.0	00000 00000 00000 00000
17 18 19 20 21	2 2 2 2 2 2 2 2 3 2 3 3 3 3 3 3 3 3 3 3	22 22 32 30 31	 SEE EE	2, 4 4 4 4 4 4 20 11 12 18 4 10 ,

ALIGNMENTS

ö

RESULT Q96DR5

g

```
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Malch 30.5%
Best Local Similarity 33.8%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9D734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09D734
                                                                                                                                                                                                                                                                                                                                                                                                                                     P79125
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9D734
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                 3
                                                                                                                             ŝ
                                                                                                                                                                     qq
                                                                                                                                                                                                             ć
                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79413; AAB38282.1; ---
SEQUENCE 243 AA; 26877 MW; 0C2D8DD45660EllC CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Verkatesh S.G., Geetha C., Gorr S.-U.;
"A member of the PSP/plunc family of BPI proteins is expressed in the human parotlid gland.";
buman parotlid gland.";
EMBL, AR43917; AAL28113.1;
SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASI,DI.LT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ11NKFVNSVINTLKSTVSSILLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AVTIETDPQTHQPVAVLRECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSIJOK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNV1SKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 KLEPVLHEGLETVDNFLKGILEKLKVDLGVLGKSSAWQLAKQEAGEAEKLLNNVISKLLP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Rovoidea;
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 333.5; DB 6; Length 243; Pred. No. 3.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 1053; DB 4; Length 249; 99.5%; Pred. No. 4.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 249
    215 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTL1 249
                                                                                                            249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                   01-DEC-2001 (TrEMBLirel, 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.4%;
34.1%;
                                                                                                                                                                                                               PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PAROTID GLAND;
                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                          TISSUE-PAROTID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P79124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P79124
                                                                                                            Q96DR5
                                                                                                                                  096DR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSP30
```

ò QQ

δ

qq ò

ò

RESULT

```
TISSUEFFICIAL TRANSMENT TO WHEELER T.T.;
Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family.";
Submitted (NV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79414; AAB38283.1;
SEQUENCE 240 AA; 26513 MW; 850611DE9E43E358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TNTD1FGLKESNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQ11NLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 VVSRLTGVRIRNVQVPDITFEATSENSA-NVLIPITADVTVSLPFLGEIVDLDLNVDLQT 145
                                                                                                                                                                                                           66 FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIE 125
                                                                                                                                                                                                                                                         126 TDPQTHQPVAVLGECASDPTSISLSIADKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                 6 LHEGLETVUNTLKGILEKLKVIJGVIQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDI 65
                                                                                                           37 LERGICTFDST1E1IFQNLKTEL----ESRCLNDVVEETQQTENSLEGLISRIFQVVNRL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 KLKSGLERGLDTFDSTIELIFQNLKTE---LESRCSDEVVEQ--QETENFLEQLISRIFQ 86
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%; Score 324; DB 6; Length 240; 33.8%; Pred. No. 1.9e-18; tive 53: Mismatches 78; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PAROTID SECRETORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 ELCPRFRELLESLDAECVEKLIGESQDTTQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 JRIFIHSLDVNVIQQVVDNPQHKTQLQT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 IRELLESLDTECIKKLIGEPOVTTOUES 239
```

```
multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIĞNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        063550:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   063550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              063550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOCCON TO THE SET TH
                                                                                                                                                                                                                                                               STRAIN-C57BL/66; PubMed-11217851; RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Rawai J., Shinagawa A., Falbata K., Yoshino M., Itch M., Ishii Y., Rawai J., Shinagawa A., Falbata K., Yoshino M., Itch M., Ishii Y., Ra Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Satio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., Satio T., Shina H., Satio T., Shina H., Gasterland T., Gissi C., King B., Kochiwa H., Ra Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Sakai K., Okido T., Furuno M., Carninci M., Wagner L., Washio T., Ra Blake J., Boffelli D., Bojunga N., Carninci M., Barsh G., Barsh G., But C., Fletcher C., Fujita M., Gariboldi M., Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Rontone P., Ring B., Ringwald M., Rodriguez I., Sakamoco N., Ra Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Winshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92129360; PubMed=1370829;
Mirels L., Ball W.D.;
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 SKLLPTNTDIFG--LKISNSL1LDVKAEPIDDGKGLNLSFPVTANVTVAGP1JGQIINLK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 ASI.DI.I.TAVT1ETDPQTHQPVAVLGECASDPTS1SI.SI.I.DKHSQ11NKFVNSV1NTI.KST 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 LGNLKSFTSLNGLLLKINNLKVLDFQAKLSSNGNGIDL/TVPLAGEASLVLPFIGKTVDIS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EPVLHEGLETVDNTLK-----GILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ESLLGE-LGSAVNNLKILNPPSEAVPQNLNLDVELLQQATSWPLAKNSIJET---LNTAD 74
                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.8%; Score 294.5; DB 11; Length 235; 32.7%; Pred. No. 4.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 AA; 24737 MW; A29D0160268DA0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 VSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK009654; BAB26418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97787; Psp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        063471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q63471
$\circ{\circ}{\circ} \circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOCCOS NEW RESTRICT OF THE STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
```

```
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 LLERVNKFRVLDLQAGLSSNGKDIDLKLPLVFEISFSLPVIGPTLDVAVSLDLLNSVSVQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 TNAQTGLPGVTLGKCSGNTDKISISLLGRRLPFVNRILDGVSGLLTGAVSILLQNILCPV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 -- LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LETVONTLKGILEKLKVDLCVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 LDILNSPSEAVAQNLNLDVGSLQQATTWPSAKDSILET---LNKV--ELGNSNGFTPLNG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEONATAL SUBMANDIBULAR GLAND PROACINAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             NEONATAL SUBMANDIBULAR GLAND PROTEIN.
0B36EC779025986E CRC64;
protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ου
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%; Score 263.5; DB 11; Length 235; 29.6%; Pred. No. 1.3e-13; tive 56; Mismatches 75; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROACINAR CELL PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                      "Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-92129360; PubMed-1370829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-98129760;
                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
MEDLINE-98129760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mirels L., Miranda A.J., Ball W.D.;
                                                                                                                                                                                                                        Mirels L., Miranda A.J., Ball W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                    multigene family.";
J. Bjol. Chem. 267:2679-2687(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 267:2679-2687(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330:437-444(1998).
                                                                                                                                                                                                                                                                                                                  Biochem. J. 330:437-444(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                          21 235 N
235 AA; 24529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 LQYLLSTMSGSA1QGLLSN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 IRIFIHSLDVNVIQQVVDN 204
                                                                                                                                                                                                                                                                                                                                            EMBL; M83209; AAC06334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M83210; AAC12783.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mirels L., Ball W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_Tax1D*10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMGB1/SMGB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins.";
Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
```

ò qq ò q

ò

```
132 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 189
                                                                                                                                                                                                                                                                  2310021H06RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09COX3;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                             09D794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09C0X3
                                                                                                                                                         090794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09C0X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DT DT
                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARAINE-21085660; PubMed-11217851;
ARAINE-21085660; PubMed-11217851;
ARAINE-21085660; PubMed-11217851;
ARAINE-21085660; PubMed-11217851;
Araine A., Para A., Fabiara K., Yoshino M., Itoh M., Ishii Y.,
Araine A., Itawa M., Nishi K., Konno H., Adachi J., Fokuda S.,
Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Anizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Anizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A. Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Coackenbush J.,
A. Sakai K., Okido T., Furuno M., Anno H., Pesole G., Quackenbush J.,
A. Sakai K., Okido T., Furuno M., Anno H., Haldarelli K., Barsh G.,
A. Barke J., Boffelli D., Peltcher C., Fullita M., Wannor C., Fullita M., Gariboldi M.,
A. Bronstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,
A. Wornstein M.J., Bult C., Fletcher C., Fullita M., Mombaerts P.,
A. Nordone P., Ring B., Ringwald M., Rodityucz I., Sakandco N.,
A. Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A. Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                            -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPI1GQI 109
                                                                                                                                            68 LKTSNSLILDVKAEPIDDGKGLNLSPPVTANVTVACPIIGQIINLKASLDLLTAVTLETD 127
                                                                                                                                                                           66 LKIKDLRILNLNHEVSPNGDEVTLKMPMALNASLSL,PARDLTTDVSISMEAITSFAIEKD 125
                                                                                                                                                                                                            128 POTHOPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 235;
                                                                         DB 11; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(4001).
EMBC. AKO10143: BAB26728.1; -
MGD: MGI:1919667: 2310074B19R1k.
SEQUENCE 235 AA; 25508 MW; B65A92860D51D8F1 CRC64;
                       91C001620761067B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
=
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 148.5; DB 1:
25.3%; Pred. No. 0.00024;
                                                                         14.6%; Score 154.5; DB 1
24.5%; Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                           42; Mismatches
       CELL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:
-:
-:
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; T1SSUE-TONGUE;
                         206 AA; 23027 MW;
                                                                                                                                                                                                                                                                                      188 IFIHSLDVNVIQUVVDNPQ 206
                                                                                                                                                                                                                                                                                                                      186 LIISN---TFHPDEISNPQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                            sest_Local Similarity 24.59
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2310074B19RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                           SEQUENCE
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9D6P2;
                                                                                                                                                                                                                                                                                                                                                                                                         09D6P2
                                                                                                                                                                                                                                                                                                                                                                                          Q9D6P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Enkuda S., Aladawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Sakuli F., Suzuki R., Tomita M., Wagner L., Washlo T., A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Batsh G., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Lyons P., Marchlonni L., Moshima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Shiata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Washia H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Washia K., Sabana Y., Kawaji H., Kohtsuki S., Marabari Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIYPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 148.5; DB 11; Length 270; 25.3%; Pred. No. 0.00029; Live 38; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB63327561D910AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 203
170 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 203
                                           PRT;
                                                                                                                                                                                                                                                                                          PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1914385; 2310021H06Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA; 29223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK009441; BAB26290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
```

Wed Aug

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AKOl0145; BAB26730.1; -..
MCD; MGI:1914385; 2310021H06Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC008429; AAH08429.1; -. SEQUENCE 484 AA; 52427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 25.3 Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAR TO DNA SEGMENT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A.
               NCBI_Tax1D=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096HK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                096HK6
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CSTBL/63; TISSUE-TONGUE;

X RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Shinagawa A., Shibata K., Yoono H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasikawa T., Saito R., Ashburner M., Baralov S., Casavant T., Racken M., Saito R., Ashburner M., Baralov S., Casavant T., Racken M., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Puuruo M., Aono H., Baldarelli R., Barsh G., Balake J., Boffelli D., Bojunga N., Carninci M., Gariboldi M., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anorone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-F., Whytaw-Ronis A., Yoshida K., Wawaji H., Kohtsuki S., Anasaki Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 LLNNVISKILPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTJPLGFULRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 LELSVKLDVTAEVYAVRDSYGRSRL-VIGDCIÝPPGSLRISLLNRLGPLQN-LIDSLTDI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 148.5; DB 11; Length 270; 25.3%; Pred. No. 0.00029; Live 38; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492A16EEBAB4A677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 LTRVIPGLVOGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAB26360.1; -. BAB26372.1; -. BAB26401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1914385; 2310021H06Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                             AK010115; BAB26710.1; -. AK009329; BAB26221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAB26343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001)
2310021H06RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310021H06RIK PROTEIN.
                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA;
                                                                                                       SEQUENCE FROM N.A.
                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK009562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK009580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK009629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK009531;
                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310021H06RIK.
               2310021H06RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09D6P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
   qq
```

```
A STRAIN-C57BL/63; TISSUE-TONGUE;

A MANAI J., SILINGAWA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Ruchi P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Saxai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sator K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

"Throttional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 LLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | ||: :|| ||: :||: ||: ||: ||: :|||: :||: :||: :||: :||: :|: :||: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 VLGKVISS-IPLLNNILDIRVTNPQLLEIGLVQSYDFHRLYVTIPLGFDLRVNTLVVGSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 INLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 13.7%; Score 145; DB 4; Length 484; 1 Similarity 23.7%; Pred. No. 0.0012; 46; Conservative 46; Mismatches 84; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
NA SEGMENT, CHR 2, MASSACHUSETTS INSTITUTE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA; 29235 MW; A86F02ABBAAFBCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08242B697284E858 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 145.5; DB 17
25.3%; Pred. No. 0.00051;
tive 38; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 LKSTVSSLLØKEICPLIRIFIHSLDVNVIQQVVD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 LTRVIPGLVQGVVCPLVNGVLSLLDVTLAHDVAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
```

3,

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 SKLLPTNTDIFGLKISNSLILDVKAEFIDDGKGLNLSFPVTANVTVAGPIIGQIINLKAS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 HTVLKY----IIWMKVTSANILQLDVQPSTYNQELVVRIPLDMVAGLNTPLIKTIVEFQMS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 LDLLTAVTIETDPQTHQPVAV-LGECASDPTS1SLSLLDKHSQ1INKEVNSVINTLKSTV 174
                                                                      72 NSLILDVKAEPIDDGKGLNLSFPVTANVTVAG---PIJGQIINLKASLDLLTAVTIETDP 128
                                                                                                        91 TANILOLOVKPSANDOELLVKIPLD --- MVAGFNTPLVKTIVEFHMTTE--AQATIRMDT 145
                                                                                                                                              129 QTHQPV-AVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VEHEGLETV------DNT1,KGTLEKLKVDLGVLQKSSAWQLAKQKAQEAEKI,LNNVI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 VLNLGPEVIQKHL/FQALKDHDATA1LQELPL-LRAMQDKSG-----SIP1LDSFV 76
                                  34 KVIKÉKLTQELKDHNATSILQQLPLLSAMREKPAGGIPVLGSLVNTVL---KHVIWLKVI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snead M.L., Villanueva J., Paine M.L., Lei Y.P., Zhu D.H., Lusis J., Xia Y.-R., Yang J.-N.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
18 KGILEKLKVDL.----GVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKIS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 129; DB 11; Length 474; 21.8%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.022;
Thes 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA; 52373 MW; 377DBFA5E736709B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VON EBNER MINOR SALIVARY GLAND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01:JUN-2001 (TrEMBLrel. 17, Last anno
1700058C13RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                       061114;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOA-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001124; LBP_BP1_CETP.
SMART; SM00328; BP11; 1.
SMART; SM00329; BP12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U46068; AAA87581.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                        188 IFIHSLDVNVIQQV 201
                                                                                                                                                                                                                                                            206 ASFNGMYADLLQLV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 SSLLQKEICPLIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 POIVKNHLCPMIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SWISS-WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D9J8;
                                                                                                                                                                                                                                                                                                                                                         061114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                          á
```

```
STRAIN-CSTBL/63; TISSUE-TESTIS;

X MEDLINE-21085660: PubMed-11217851;

XR Awawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa T., Iazwa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Rosole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Stati K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

A Blake J., Bóffelli D., Bölunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Usons P., Marchionni L., Masahima J., Mazzarelli J., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N.,

A Sasaki H., Sato K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AEPIDDGKGLNLSFP---VTANVTVAG-----PIIGQIINLKASLDLLTAVTIETDPQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 -----DCGGIQMAFPKEWFSANITLEFDIEFKLPFNSNIIKTHACMGLTAESWLEKDEFG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 HQPVAVLGECASDPTSISLSL-LDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LLDRENVSGTVAPGMVGWELGGMNFQQQQEISIN1-----TNVQL-------101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 ILEKLKYDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSL1LDVK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49G10.6 (SIMILAR TO MURINE VON EBNER MINOR SALIVARY GLAND PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 126; DB 11; Length 232; 21.2%; Pred. No. 0.016; tive 43; Mismatches 73; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tracey A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AI,121901; CAC03550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25713 MW; 0D52D24A3076D5DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
EMBL; AKO06829; BAB24760.1; -.
MGD; MGI:1920638; 1700058C13Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 THSLDVNVIQUVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 LRULDVKLLKGLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM 1) (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DJ1187J4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BQP8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09BQP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09BQP8
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               August 6, 2002, 16:52:52; Search time 138.55 Seconds (without aliquments) 172.363 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDSI/gcgdata/hold-geneseqq/geneseqp-embl/AA1996.DAT:*/SIDSI/gcgdata/hold-geneseqq/geneseqp-embl/AA1996.DAT:*/SIDSI/gcgdata/hold-geneseqq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/hold-geneseqq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/hold-geneseqq/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
/SIDEI/goddata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                             1 KLEPVLHEGLETVDNTLKGI.......NVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                          US-10-020-139-2_COPY_35_249
                                                                                                                             OM protein · protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapup 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                    1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                       Sedneuce:
                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                        Title:
```

	Description	Human parotid secr	Human parotid secr	Human PRO1025 prot	Human secreted pro	Human secreted pro	Human protein segu	. Peptide #8941 enco	Human brain expres	Human bone marrow	Peptide #9264 enco	Mouse 28.6 kDa sec
	ID	AAW69221	AAW60682	AAB24069	AAB25765	AAB75351	AAM25745	ABB41435	AAM62308	AAM75111	AAM35227	AAE05367
	DB	19	19	21	21	22	22	22	22	22	22	22
	Length	249	249	249	249	249	260	50	50	50	20	278
₩ P	Query e Match Length DB I	100.0	100.0	100.0	100.0	100.0	96.4	23.2	23.2	23.2	23.2	17.2
	Score	1061	1061	1061	1061	1061	1023	246	246	246	246	182.5
	Result No.	-	2	8	4	2	9	7	αο	σv	10	11

(HUMA-) HUMAN GENOME SCI INC

23-DEC-1996;

Duan R, Ruben SM;

97WO-US23522. 96US-0034429.

						9
12	178	9		0.0		Human secreted pro
0 4	170	2		, c	AAV60164	acid sec
+ u	178	2 4		, ,	AA139019	secreted
7	0 / 1	⊃ v		2 C	AAU29210	PRO E
17	178	S CO		22	AAM39721	n polypept
. 20	178	9		22	AAB97366	Human LUNX protei
19	178	16.8		2.5	AAM92209	Human digestive sy
2.0	178	9		22	AAM41507	Human polypeptide
21	168	LO L		55	AAM92212	Human digestive s
22	791	က :		77	AAM92214	Guman MOVAN prote
m •	146	~ .		77	AAM4 / 220	Human NOVA prote
47 7.0	0 4 1	7 (7 .	AAM4/214	Human neurotransm
2,0	140	$^{\circ}$		22	AAG63976	Amino acid sequen
27	147	nm		21	AAY99375	Human PRO1357 (UN
28	144	3		22	AAU29163	Human PRO polypep
29	144	m		22	AAB87564	Human PRO1357. H
3.0	144	3		22	AAB66124	Protein of the in
31	143	m		27.7	ABG08520	Novel numan diagn
32	108	\circ		7.7	AAY86219	Human Secreted pr
ian c ian e		$\supset c$	-	7 7	AAB583/8	Tobamovirus renli
ა ი 4 դ	0 G	n c	-1	, ,	AANGGGG AAII35585	Haemophilus influ
n w		0 0		10	AAU34151	Staphylococcus au
3.6	94.5	0.00		22	AAU37067	Staphylococcus au
88		σ.		22	AAU34336	Staphylococcus au
3.6		8.9		22	AAU37370	Staphylococcus au
40	46	8.9		22	AAU68518	Human novel cytok
41	65	8.7	•	23	AAB15945	E. coli proliterat
2 -	2.5	о ч ю	•	70	AARSOLO AAME8387	Clostridium diffi
7 4	- G	ο α	•	22	ARB64187	Drosophila melano
4 4	68) &) 4.	1057	22	AAG67419	2
					ALIGNMENTS	
3ULT 4692 A	1 21 AW69221 st	tandard;	d; Protein	in;	249 AA.	
Ø						
16	-0CT-1998	3 (f)	rst entry)	(Å)		
	Human parot	p	secretory	protein	ein.	
XX KW Parot: KW non-ir	id:	secretory pre diagnosis	e c	in; k sorde	cein; hPSP; digestive disorder; disorder; immune system disorder	er; endocrine disorder; rder; cancer; human;
OS Homo	o sapien	w				
52 C	ey		Location	o√our	lifiers	
	tide		118 /note= '	"sigr	nal peptide"	
Δ.	rotein		19249 /note= '	"matı	19. 249 /note= "mature hPSP"	
	WO9828420-	-A1.				
ć	- 0					
20	- 10L - 199	20				

```
This sequence is the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, amplification or immunosis of the salivary gland, thymus and application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial antiparasitic and antiviral apenists and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secretory tissue; gastrointestinal tissue; HPSP, Sjorgen's syndrome; Graves disease, thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 tntdifglkisnslildvkaepiddgkglnlsfpvtanvtvagpiiggiinlkasidllt 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1061; DB 19; Length 249; 100.0%; Pred. No. 7.7e-93; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parotid secretory protein; human; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 eicplirifinsldvnviqqvvdnpqhktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parotid secretory protein (HPSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60682 standard; Protein; 249 AA.
                                                                                                                                              Claim 16; Fig 1; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US20651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.8
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hPSP-binding proteins.
WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 AA:
                         N-PSDB; AAV44759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9821329-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW60682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ρp
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
```

```
This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically Lo, and modulate activity of HPSP are used to that bind specifically Lo, and modulate activity of HPSP are used to treat and autofinmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, of gastrointestinal tract or pancreas, Sjorgan's syndrome, of Graves disease, thyroidilis, insulin-dependent diabetes, pancreatitis, ucerative colitis, Crohn's disease and atrophic gastritis. Host cells ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may conducted call or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; noctropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antianalyogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1061; DB 19
ilarity 100.0%; Pred. No. 7.7e-93;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 eicplirifihsldvnviqqvvdnpghktglqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1025 protein sequence SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB24069 standard; Protein; 249 AA
                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1A-C; 65pp; English.
              96US-0749288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2001 (first entry)
                                                             (INCY-) INCYTE PHARM INC.
                                                                                                         Bandman O, Goli SK;
                                                                                                                                                     WPI; 1998-297933/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
ses 215; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA;
                                                                                                                                                                              N-PSDB; AAV37699.
                 14-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB24069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

ö

121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180

> g ò

AAB25765 standard; Protein; 249 AA.

Human secreted protein SEQ ID #77.

28-NOV-2000 (first entry)

AAB25765;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours of e.g., renal, ilver, Kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AACS8242 to AACS836 represent pCR primers and hybridisation probes used in the isolation of the human PRO sequences. AACS836 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1005, PRO1003, PRO1003, PRO1003, PRO1003, PRO1003, PRO1003, PRO1003, PRO3111, PRO1003, PRO1003, PRO334, PRO100017, PRO1000, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleoides are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that binds to
hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1061; DB 21; Length 249; 100.0%; Pred. No. 7.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker KP, Goddard A, Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 61; Fig 26; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0143048.
99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0141037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US30911.
                                                                                                                                                                                                                                                                                                                                                                                06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2000; 2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 215, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-572270/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC58379
                                                                                                                                                                                                                               40200053755-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999;
20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe CK,
                                                                                                                                                                                                                                                                                                         14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

Bougueleret L, Dumas J, Duclert A;

(GEST) GENSET.

WPI; 2000-442637/38.

N-PSDB; AAA87727.

99WO-IB02058. 98US-0113686. 99US-0141032.

20-DEC-1999; 22-DEC-1998; 25-JUN-1999;

29-JUN-2000.

Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;

septic shock; impotence.

WO200037491-A2.

Homo sapiens.

```
This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87125-A87774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the Invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted fortiens. The cDNAs may also be useful in diagnostic, foremsic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, and besity, mitchondrioproprofiles, and immunological demontain, hyperlipidaemia, septic shock and impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Figure 10; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
NO COURT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
```

qq

qq

```
61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH99686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
                                                                                                                                                                                                                                                            AAM25745;
                                                                                                                                                                                                              AAM25745
                                                                                                                                                                                                  RESULT
                                qq
                                                                                              qq
                                                                                                                           ò
                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                     .;
O
                                                                                                                                         61 TNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINEKASLDILT 120
                                                                                                                                                                                                  121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                95 tntdlíglkisnslildvkaepiddgkglnlsfpvtanvtvagpiiggiinlkasldll 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLEPVI,HEGLETVDNTLKGILEKLKVDI,GVI,QKSSAWQLAKQKAQEAEKILINNVISKI,LP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                 1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNV1SKLLP 60
                                                                                                 49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to 49 Secreted proteins and the cle encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1061; DB 22; Length 249; 100.0%; Pred. No. 7.7e-93; tive 0; Mismatches 0; Indels 0;
                                                     ..
O
                       DB 21; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; prevention; treatment; diagnosis; disease;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J, Bougueleret L, Jobert S;
                                                      .;
0
                          100.0%; Score 1061; DB 21
100.0%; Pred. No. 7.7e-93;
                                                                                                                                                                                                                                                                           215 eicplirifilisidvnviqqvvdnpqhktqlqtli 249
                                                                                                                                                                                                                                                            181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 281; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                  AAB75351 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000; 2000WU-IB00951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99115-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0469099
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215; Conservative
                            Query Match
Best Local Similarity 100.0
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-071487/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0200100806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                               AAB75351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                             qq
                                                                                                                  qq
                                                                                                                                                                          qq
                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                   q
                                                                                       ô
                                                                                                                                                δ
```

셤

```
AMM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antinheumatic; antiartiate; mmunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabatichant immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianapy/tactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antilnflammatory; antirheumatic; antiarthritic; immunosuppressive; antiboterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialergic; antiasthmatic; antidiabetic; cytostatic;
95 tntdifglkisnslildvkaepiddgkglnlsfpvtanvtvagpilgginlkasidlt 154
                                                                 121 AVTIETDPOTHOPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                          Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
                                                                                                                                                                 181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                            215 eicplirifihsldvnviqqvvdnpqhktqlqtli 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ 1D NO:1260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 260; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                AAM25745 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999; 9903-0471275.
21-JAN-2000; 20000S-0488725.
25-APR-2000; 20000S-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 2001-457603/49.
```

Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English

..

```
ó
production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HV and lungal infections, autoimmunity, genetic diseases, heematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immundeficiency, eczema, allengic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                 46 Klepvlhegletvdntlkgilekikvdlgvlgkssawglakgkageaekllnnviskilp 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTDIFGLK | SNSL JL, DVKAEP | IDDCKGLNLSFPVTANVTVAGPIJGQIINLKASLDLLT | 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            1 KLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                           96.4%; Score 1023; DB 22; Length 260; 96.7%; Pred. No. 3.4e-89;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                          3.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 EICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eicplirifihsldvnviggvvdnpghktglgtli 260
                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB41435 standard; Peptide; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                            neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                        260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                              208;
                                                                                                                                                                                                              Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB41435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
```

```
probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                     measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                            printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 34413; 650pp + Sequence Listing; English.
                                            The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe
                                                                                                                                                                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 piigqlinlkasldlltavtietdpqthqpvavlgecasdptsislslld 50
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                     23.2%; Score 246; DB 22;
100.0%; Pred. No. 2.8e-16;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                              23.25.
100.0%; Pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM62308 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                               50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM62308;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
8 X C C C C C C C C C C X S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
```

ø

```
AAM35227 standard; Protein; 50 AA.
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AA;
                                                                                          qenetic disorder.
                                                                                                                                WO200157272-A2.
                                                                                                                                                                                            04-FEB-2000;
                                       17-OCT-2001
                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                  AAM35227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE05367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ 1D NO: 35417; 658pp + Sequence Listing; English.
                                                  .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                      104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.2%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 2.8e-16;
                                                                                23.2%; Score 246; DB 22; Length 50;
                                                  Indels
                                                                                                                                                                                                                                     microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ....
                                   100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                           AAM75111 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                 2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                         200005 - 0180312.
                                                                                                                                                                                                                                                                                                                                                                                           2000015-0236359.
                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AA;
 50 AA;
                                                                                                                                                                                                                                                                             WO200157276-A2.
                                                                                                                                                                                                                                                          HOMO Sapiens.
                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2000;
                                                  50;
                                                                                                                                                                 AAM75111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
  Sequence
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                   Matches
  S
                                                                        ò
                                                                                           q
                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

AAM35227

```
The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse, cytostatic; antiinflammatory; immunoregulatory; tissue integrity; wound healing; immune response; vaccine; cancer; asthma; alleggy; cell trafficking; therapy; 28.6 kDa secreted protein.
Peptide #9264 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.2%; Score 246; DB 22; Length 50; 100.0%; Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 35496; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE05367 standard; Protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse 28.6 kDa secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WP1; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
```

AAY06408

```
The proteins which play a major role in induction of growth, cell migration of proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynuclectides of the invention are useful in genome and physical mapping, in positional cloning of are useful in genome and physical mapping, in positional cloning of one-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as immunoregulatory and anti-inflammatory molecule, as a part of a part of a vaccine or anti-cancer readenert, and as a starget for antagonists in the treatment of the invention, for tissue and neural recemberation, to promote or history the invention, for tissue and neural recemberation, to promote or history
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is 28.6 kDa protein, a secreted protein from mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses novel polynucleotides and their corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 92; 101pp; English.
                                                                                                                                                                                                                         21-DEC-2000; 2000WO-NZ00256.
                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2000; 2000US-0724864.
                                                                                                                                                                                                                                                                                                                                    99US-0171678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watson JD, Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-425665/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD10135
WO200148192-A1.
                                                                                                                                                                                                                                                                                                                              23-DEC-1999;
                                                                                                               05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
```

```
90 igileniplidviksgggnsnglvggilgkltssvpllnnildikltdpgileiglvgsp 149
                                                                                                                                                                   85 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQ--THQPVAVLGECAS 142
                                                                                                                                                                                                          150 dghrlyvtiplgltlnvnmpvvgsllglavklnitaevlavkdnggrih---lvlgdcth 206
                                                                                                                                                                                                                                                       143 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISKL---LPTNTDIFGLKISNSLILDVKAEPID 84
      DB 22; Length 278;
                                           88; Indels
Query Match 17.2%; Score 182.5; DB 3
Best Local Similarity 24.5%; Pred. No. 3.1e-09,
                                        45; Mismatches
                                           Conservative
                                                                                                                                                                                                                                                                                                                                            203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                    266 ellihglq 273
                                        46;
                                        Matches
                                                                                                                                                                      ò
                                                                                                                                                                                                          pp
                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                          δ
```

RESULT

```
nijo 17. The sequence is predicted from a full-length cDNA clone (see AAX59356) isolated from a human adult brain (thalamus) CDNA library. The invention provides CDNA clones (see AAX59355.8) encoding novel secreted proteins (see AAX60404-10) of the human cestis, brain and foetal kidney. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data are provided. Suggested activities include nutritional, vytokine, cell provided. Suggested activities include nutritional, vitokine, cell provided activities include nutritional, closed activities as active or immunosuppressive, heematopoiesis regulating, tissue growth, activin or inhibin, chemotactic or chemokinetic, heemostatic, thrombolytic, receptor/ligand, antiinflammatory, cacherin or tumour invasion suppressor, and tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 igilenlplldilkpgggtsggllggllgkvtsvipglnniidikvtdpgllelglvqsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 DGKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel human secreted protein, termed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
                                                                                                                                                     Secreted protein; nh796_1; human; brain; thalamus; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Indels
                                                                                                                                                                                                                                                                                     /note= "predicted leader/signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins-Racie LA, Jacobs K, LaVallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merberg D, Steininger RJ, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

16.8%; Score 178; DB 20;
Best Local Similarity 24.5%; Pred. No. 7.5e-09;
Matches 46; Conservative 44; Mismatches 92;
                                                                                                                                                                                                                                                                                                                             "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; Page 96-97; 100pp; English.
                                                                                                                                                                                                                                                    Location/Qualifiers
AAY06408 standard; Protein; 256 AA,
                                                                                                                 Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0222653.
98US-0070346.
                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US27903
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                           20..256
                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-419350/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX59356
                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               W09935252-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ,
                                                                          20-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999.
                                                                                                                                                                           diaqnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCoy JM,
                                      AAY06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity.
                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                           Protein
                                                      Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

qq ò q

Best Local Similarity

```
Sequences are supposed to their sequences. The present invention relates to detection of a target LST70 polynucleotide that comprises treating a test sample with at least one LST70-specific nucleic acid that has at least 50 percent identity with any of the sequences (AAX00801-09) which are fragments derived from various clones of LST70 gene. The LST70 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease. Particularly detection of LST70 polynucleotide, LST70 antigens, or anti-LST70 antibodies is indicative of disease. Cells transformed with an expression system comprising the LST70 nucleic acid sequences are used to express recombinant polypeptides. The polypeptides are used to raise Ab and for drug screening. LST70 related nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used to isolate related sequences; as standards and reagents in sasays; as targets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or triplex-forming agents, ho can be used to deliver therapeutic agents to LS170-expressing cells; directly as therapeutic agents (by neutralising LS170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design.
                                      144 PTSISLSLLDKHSQ1-INKFVNSVINTLKSTVSSLLQKEICPLIKIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAW95463-471 represent LS170 polypeptide fragments which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LS170 gene; in vivo imaging; lung disease; cancer; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New LS170 nucleic acid from lung tissue - useful for detecting, monitoring, preventing and treating lung disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Cohen M, Colpitts TL, Friedman PN;
dosen, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 96-97; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95463 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US11601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0049183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LS170 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Granadosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-060335/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billing-medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AA;
                                                                                                                                                            203 DNPQHKTQ 210
                                                                                                                                                                                                                                        244 nmlihglg 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX00809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts-rapp L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09856951-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW95463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                         AAW95463
                                                                                                                                                                                                                                                                                                                                                              RESULT
```

16.8%; Score 178; DB 20; Length 256;

Query Match

```
Lung specific genes for developing products for diagnosing, monitoring,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is encoded by a lung specific gene, designated Lng110, clone ID 135520, gene ID 236760. The specification describes methods for diagnosing the presence of lung cancer in a patient. The method comprises measuring levels of lung specific genes in cells, tissues or bodily fluids, and comparing the level to that of a normal human control. The methods can be used for diagnosing, monitoring, staging or prognosticating lung cancer, especially metsatatic lung cancer. Antibodies against proteins encoded by lung specific genes can be used for imaging or, when conjugated to a cytotoxic agent, for
                                                                                                                                                    85 DOKGENESFPVTANVTVAGPIIG-QIINEKASEDELTAVTIETDPQTHQPVAVEGECASD 143
                                                                                                                                                                                              144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                               65 lgilenlplldilkpaggtsggllggllgkvtsvipglnniidikvtdpgllelglvqsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                               28 LGVLOKSSAWQLAKQKAQEAEKILLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung specific gene; lung cancer; metastatic lung cancer; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%; Score 178; DB 21; Length 256; 24.5%; Pred. No. 7.5e-09; tive 44; Mismatches 92; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       staging, prognosticating, imaging and treating lung cancer
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of lung specific protein Lng110.
Pred. No. 7.5e-09;
        24.5%; Pred. No. iv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun Y, Recipon H, Macina RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 35-36; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAY69164 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US16247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0095233
                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (first entry)
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DIAD-) DIADEXUS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195589/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 AA;
                                                                                                                                                                                                                                                                  203 DNPQHKTQ 210
                                                                                                                                                                                                                                                                                              244 nmlihglq 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ61165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200008206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000.
                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang F,
                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                   AAY69164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                 δ
                                                                                             q
                                                                                                                                  ŝ
                                                                                                                                                               q
                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                q
```

```
The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifheumatic; antitumor; antituder; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; manumor; severe combined immunodeficiency; Severe combined immunodeficiency; Stop. tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; Huntingon's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                  144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                           85 DGKGLNLSFPVTANVTVAGPTIG-QIINEKASLDLETAVTIETDPQTHQPVAVLGECASD 143
                                                                                              125 dghrlyvtiplgiklqvntplvqasllrlavklditaeilavrdkqerihl-vlgdcths 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiantrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lavallie E, Collins-racie LA,
J, Steininger RJ, Spaulding V,
Merberg D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 497-498; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system disorders (e.g. stroke) -
                                                                                                                                                                                                                                                                                                                                                      AAU39019 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein nh796_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001; 2001WO-US09369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2000; 20000S-0539330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2000; 2000US-0729674.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food supplement; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs K, McCoy JM, La
Treacy M, Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639363/73.
                                                                                                                                                                                                                  203 DNPQHKTQ 210
                                                                                                                                                                                                                                                     244 nmlihglq 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS59237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175068-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                            AAU39019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark H,
                                                                                                                                                                                                                                                                                                            RESULT 1:
AAU39019
                                                                                              g
                                                                                                                                                                        q
                                                                                                                                                                                                                  ò
```

```
4
systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-lost diseases (COHB), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers, as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system,
                                                                                                                                                                                                                                                                                          sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 DGKGLNLSFPVTANVTVAGPIIG-QIINLKASLDLLTAVTIETDPQTHQPVAVLGECASD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 PTSISLSLLDKHSQI-INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 pgslqislldglgplpigglldsltgilnkvlpelvggnvcplvnevlrglditlvhdiv 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 igileniplidilkpgggtsggliggligkvtsvipglnniidikvtdpgllelglvgsp 124
                                                                                                                                                                                                            Alzheimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel eg. stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 LGVLQKSSAWQLAKQKAQEAEKLLNNVISK---LLPTNTDIFGLKISNSLILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                       proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 178; DB 22; 24.5%; Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6, 2002, 16:52:52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNPOHKTQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 nmlihglq 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Job time: 334 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
```

```
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-700-548-4
                                                                                                                                                                                                                                                                                                              80.5
80.5
80.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                       (without alignments)
102.528 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                             1 KLEPVLHEGLETVDNTLKGI........nvIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Sequence 2, Al Sequence 98, Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98,
Sequence 98,
Sequence 6, A
Sequence 2, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4,
                                                                                                                           August 6, 2002, 16:53:52; Search time 51.22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6G_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FCOMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                    Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08 480-604A-6
US-08 495-496A-6
US-08 495-136-6
US-08 915-136-6
US-08 915-136-4
US-08 990-140-4
US-08 990-140-4
US-08 990-140-4
US-08 990-140-4
US-08 790-912-2
US-08 180-111-2
US-08 838-11-2
US-08 8372-105-98
US-08 8372-105-98
US-08 8372-105-98
US-08 8372-105-98
US-08 8372-105-98
US-08 8372-105-98
US-08 844-99
US-08 844-99
US-08 844-99
US-08 847-3344-99
US-08 847-3344-99
US-08 847-334-39
                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
GenCore version 4.5
                                                                                                                                                                                                                                                                                                                                                                        231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                   US-10-020-139-2_COPY_35_249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551
2710
2710
2710
1051
1057
198
907
907
940
1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4481
1997
4481
4481
4481
4481
4481
4481
481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                      OM protein
                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                               Run on:
```

```
Appli
Appli
                                                                          Appl
                                                                                                                            , Appl
Appli
Appli
                                                                                       Appl
                                                                                                                                                                                                                                                                                                                                                     Para-Influenza Virus-Containing Vaccines for Preventing Porcine Reproductive and Respiratory Syndrome
                                                                                                                                                                         Sequence 98,
Sequence 4, A
Sequence 4, A
                                                                                                                                                                                                                                                                                                                                                     Heinen, Ernst; Schmeer, No. 5910310bert; Herbst, Werner
                                                  Sequence 98,
                                                                                                                                                                                                     Sequence 4,
Sequence 2,
                                                                         Sequence 5
                                                                                                                                       Sequence (
                                      Sequence
                       Sequence
                                                               Seguence
                                                                                                   Sequence
                                                                                                               Sequence
                                                                                                                            Sequence
                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 2; Length 551;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette, 3.50 inch, 1.4 Mb storage
                   US-08-955-660-2
US-08-195-660-2
US-08-119-263-98
US-08-224-480-98
US-08-431-517F-11
US-09-146-65-98
PCT-US94-02465-98
PCT-US94-07831-4
PCT-US95-00656-98
PCT-US95-0069-98
PCT-US95-0069-98
US-08-785-431-4
US-08-785-431-4
US-08-785-431-4
                                                                                                                                                                                                                                                                                                                                                                                                                              Sprung Kramer Schaefer & Briscoe
660 White Plains Road
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintos, 6500
OPERATING SYSTEM: System 7.5
SOFFENT APPLED THE SYSTEM: System 7.5
SOFFENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,548
FILING DATE: 30-AUG-1996
CLASSIFFICATION DATA:
APPLICATION NUMBER: PCT/EP95/00642
FILING DATE: 22-FEB-1995
FILING DATE: 07-MAR-1994
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE 44 07 489.1
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08700548 Patent No. 5910310 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33.141
REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (914) 332-170
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 551 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Heinen, Erns
TITLE OF INVENTION: PAR
TITLE OF INVENTION: PRE
TITLE OF INVENTION: SYN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ZIP: 10591-5144
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-700-548-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: boc ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
```

```
215 1 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>a</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                            80 LOPI-GENLETIRNOLIPTRRRRFACVVICLAA-LGVATAAQVTAAVALVKANKNAAAI 137
                                                                                                                      50 L-LANVISKLLPTNTD1FCLKISNSL1LDVKAEPIDDGKGLNLSFPVT-ANVTVAGP11G 107
                                                                                                                                                             138 LNLKNAIOK---TNTAVADV-VQATQSLGTAVQAVQDHINSVVSPAITAANCKAQDAIIG 193
                                                                                                                                                                                                     108 QIINLKASLDILTAVTIETDPQTHQPVAVLGECASDPTSIS---LSLLDKHSQIINKFVN 164
                                                                                                                                                                                                                                          194 SILNL----YLTELLTTIFHNQITNP-----ALSPITIQALRILLGSTLPTVVEKSFN 24]
                                                                                                                                                                                                                                                                                      165 SVINTLKSTVSSLLQKELCPL-----IRIFIHSLDVNVIQQVVD-----NPQH 207
                                                                                                                                                                                                                                                                                                              99; Indels 52; Gaps
                                       2 LEPVLHEGLETVDNTL-----KGILEKLKVDLGV---LQKSSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADISE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: TAKEN TO THE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATHENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 MONTGOMERY STREET, SUITE 2200
  Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/422,711 FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: US 08/161,907
02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDIEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/985,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/429.791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08480604A Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-APR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KINK,
                                                                                                                                                                                                                                                                                                                                                                       208 KTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                              302 MAQEPTRV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-480-604A-6
  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
Matches
                                         ô
                                                                            Db
                                                                                                                      ò
                                                                                                                                                           q
                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                            QQ
```

```
959 NTLNAAFFIQSLIDYSSNKDVLNDLSTSVKVQLY --- AQLFSTGLNTIYDSIQLVN---- 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012 LISNAVNDTINVLPTITEGI-----PIVSTILDGINEGAAIKELLDEHDPLLKKELEAK 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 IINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVN-VIQQVVD--NPQHKTULQTL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             842 KLEPVKNIIHNSIDDLIDEFNLLENVSDELYELKKLNNLDEKYLISFEDISKNNSTYSVR 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 NVTVAGPIIGQIINLKASLDLLTAVTIETUPQTHQPVAVLGECASUPTSISLSLLDKHSQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLEPVLHEGLETVDNTLK -- GILEKLKVDLGVLQK ------SSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 LLN--NVISKI,LPTNTDIFG------LKISNSI,ILDVKAEPIDDGKGLNLSFPVTA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.6%; Score 91; DB 1; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8; Matches 50; Conservative 51; Mismatches 98; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VACCINE FOR CLOSTRIDIUM BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
REFERENCE/DOCKET NUMBER: OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: US/U8/405,496A
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US 08/329,154
25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/161,907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08405496A Patent No. 5919665
GENERAL INFORMATION:
                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8738
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FO
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 16-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLUGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-480-604A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1066 V 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-405-496A-6
```

```
959 NTLNAAFFIQSLIDYSSNKDVLNDLSTSVKVQLY---AQLFSTGLNTIYDSIQLVN---- 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 IINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    902 FINKSNGESVYVETEKEIFSKYSEHITKEISTIKNSIITDVNGNLLDN---IQLDHTSQV 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 NVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLEPVLHEGLETVUNTLK--GILEKLKVDLGVLQK------SSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 LLN--NVISKLLPTNTDIFG------LKISNSLILDVKAEPIDDGKGLNLSFPVTA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.6%; Score 91; DB 2; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8; Matches 50; Conservative 51; Mismatches 98; Indels Andthes 98; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                 ATJUMENT TO ATTACK TO ATTACK THE TO ATTACK TO 
Arplication NUMBER: US 07/429,791 FILING DATE: 31-0CT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08915136 Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: protein US-08-405-496A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1066 V 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 1 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-915-136-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       òλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
959 NTLNAAFFIQSLIDYSSNKDVLNDLSTSVKVQLY---AQLFSTGLNTIYDSIQLVN----1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1012 LISNAVNDTINVLPTITEGI-----PIVSTILDGINLGAAIKELLDEHDPLLKKELEAK 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 IINKFVNSVINTLKSTVSSLLOKEICPLIRIFIHSLDVN-VIQQVVD--NPQHKTQLQTL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 NVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLEPVLHEGLETVDNTLK--GILEKLKVDLGVLQK-----SSAWQLAKQKAQEAEK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 LLN--NVISKLLPTNTDIFG------LKISNSLILDVKAEPIDDGKGLNLSFPVTA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Weiser, Jeffrey N.
APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.6%; Score 91; DB 4; Length 2710; Best Local Similarity 20.7%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Conservative 51; Mismatches
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/007
FILING DATE: 04-DEC-1993
APPLICATION NUMBER: US 07/007
PRIOR APPLICATION NUMBER: US 07/007
                                                                                                                                                                                                                                                                                                   FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                   APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08790912
Patent No. 5976542
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: OP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       irrE: amino acid

TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-915-136-6
                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennsylvania
                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1066 V 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 I 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-790-912-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
```

```
506 TTKDVSCLHSKLDRKKAVDQHINAEAQDIFGKNLNSLFNNMEELIKDGSSKQKAMLEVHKT 565
                                                                                                                                                                                                           105 ILGQIINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKF- 162
                                                                                                                                                                                                                                                      566 LFGNLLSSSVSALDTITTV------ALGSLTSIPENVSTHV----SQIFNMIL 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 FPVT-ANVTVAGPIIGQ--IINLKASLDL-LTAVTIETD------PQTHQPVAVLGECAS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 THTDIFGL--KISNSLILDVKAEPIDD--GKGLNLSF-------PVTANVTVAGP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 83.5; DB 1; Length 198; Best Local Similarity 18.1%; Pred. No. 0.51; Matches 32; Conservative 44; Mismatches 76; Indels 25; Gaps
                 10 LETVDNTLKGILEKLKVDLCVLQKSSAWQLAKQK-----AQEAEKLLNNVISKLL----P 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 AQEAEKLLNNVISKL-LPTNTDIFGLKISNS-----LILDVK-----AEPIDDGKGLNLS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 SQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipopolysaccharide Binding Protein Derivatives 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                      163 -----VNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVN 196
                                                                                                                                                                                                                                                                                                                                          609 KEQSLAAESKTVLQELINVLKTDLLSSLEMILSPTV---VSILKIN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27129/32137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/261,660A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY; United States of America 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 49, Application US/08261660A
Patent No. 5731415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27 THUECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Lip
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-261-660A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-261-660A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILESHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qu
                                                                                                                                                                                                                                                           ą
                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                               q
                                                                                                                  ô
                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 -----KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTA-V 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   794 KADNSKISNSSF-----KGRIVN-SYETKAPYNIGG-LVGQLTGINALVDKSKATI 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Mismatches 79; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  743 TVENLTLKDVNISGKTDIGAL-----ANEANNATRINNVHVDGVLAGERGIGGLVW 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 TVDN-TLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKILPTNTDIFGL-- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 26.5%; Score 90.5; DB 2; Length 1861;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%, Score 89; DB 4; Length 1057; Best Local Similarity 23.0%; Pred. No. 1.6; Matches 52; Conservative 35; Mismatches 79; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TIETD-PQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               843 TISSNADSTNQTVGGLA------GLVEKDALISNSYAEGNINNVK 881
                                                                                                                          SOFTWARE: Patenth Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790.912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                      FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION IMPA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09541782
Patent No. 6284480
Patent No. 6284480
PAPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Bakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFRENCE/DOCKET NUMBER: 7600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2991
TELEFAX: (215) 567-2991
                                                                              COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1861 amino acids
                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-790-912-4
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: H.sapiens
US-09-541-782-10
                      19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831-494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-541-782-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
```

.. &

```
, aa
.
                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruben, Steven M.
APPLICANT: Sonenberg, Nahum
APPLICANT: Sonenberg, Nathalie
APPLICANT: Methot, Nathalie
APPLICANT: Methot, Nathalie
APPLICANT: Methot, Nathalie
APPLICANT: Methot, Nathalie
TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) Polynucleotides
TITLE OF INVENTION: (as amended)
TITLE OF INVENTION: (as amended)
TITLE OF INVENTION: (as amended)
CURRENT APPLICATION NUMBER: US/09/546,238
CURRENT FILING DATE: 2000-04-10
COURTENT FILING DATE: US 60/033,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 HPPLFLLCLQQLAKLQDREWLTELFQQSKVN--MQKMLPEIDQNKD-------713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 KAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714 RMLEILEGKGLSFLFPL------LKLEKELLKQIKLDPSPQTIYKWIKDN 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QPVAVLGECASDPTS1SL----SLLDKHSQ11N 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 ISPKLHVDKGFVNILMTSFLQYISSEVNPPSDETDSSSAPSKEQLEQEKQLLLSFKPVMQ 817
                                                                                                                                                                                                                                                                            APPLICANT: Somenberg, Nahum
APPLICANT: Methot, Nathalie
APPLICANT: Methot, Nathalie
APPLICANT: Rom, Eran
TITLE OF INVENTION: eIF4GF-like Protein (p97) Genes
FILE REPERENCE: 1488.0700001
CURRENT APPLICATION NUMBER: US/08/990,140A
CURRENT FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: US 60/033,151
EARLIER PILING DATE: 1996-12-13
NUMBER OF SEO ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 EGLETVDNTLKGILE-----KLKVDLGVEQKSSA------36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ------WQLAKQKAQE-----AEKLLNNVISKLLP---TNTDIFGLKISNSL1LDV 78
143 DPTSISLSLLDKHSQIINKFVNSVIN----TLKSTVSSLLQKEICPLIRIFIHSLDV 195
                                           138 DIADVEVDMSGDLGWLLNLFHNQIESKFQKVLESRICEMIQKSVSSDLQPYLQTLPV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 19.0%; Pred. No. 4.6;
Matches 55; Conservative 41; Mismatches 62: Indele 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 KFVNSVINTLKSTVSSLLQKEI-C-----PLIRIFIHSLDVNVIQQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 KFLHDHVDL---OVSALYALQVHCYNSNFPKGMLLRFFVHFYDMEIIEE 863
                                                                                                                                                       . Sequence 4, Application US/08990140A
; PaterL No. 6093795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09546238
Patent No. 6316225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen, Henrik S.
Ruben, Steven M.
                                                                                                                                                                                                                                 APPLICANT: Olsen, Henrik S. APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                 RESULT 8
US-08-990-140-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-990-140-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-546-238-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                           g
  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEMERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins
TITLE OF INVENTION: Use of said Genes and Proteins
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/08/810,712G
CURRENT FILING DATE: 1997-03-03
EARLIER TILING DATE: 1994-10-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             670 HFPLFLLCLQQLAKLQDREWLTELFQQSKVN--MQKMLPEIDQNKD------713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 KAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 ...-H-----SLLDKHSQIIN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 EGIATSDNFMQAFLNVLDQCPKLEVDIPLVKSYLAQFAARAIISELVSISELAQPLESGT 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 ISPKLHVDKGFVNILMISFLQYISSEVNPPSDETDSSSAPSKEQLEQEKQLLLSFKPVMQ 817
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 EGIATSDNFMQAFLNVLDQCPKLEVDIPLVKSYLAQFAARAIISELVSISELAQPLESGT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 HFPLFLLCLQQLAKLQDREWLTELFQQSKVN--MQKMLPEIDQNKD------746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQT----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747 RMLEILEGKGLSFLFPL-------LKLEKELLKQIKLDPSPQTIYKWIKDN 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 ------WQLAKQKAQE-----AEKLLNNVISKLLP---TNTDIFGLKISNSLILDV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 EGLETVDNTLKGILE-----KLKVDLGVLQKSSA-----36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 19.0%; Score 83.5; DB 4; Length 907; Matches 55; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 KFVNSVINTLKSTVSSLLQKEI-C-----PLIRIFIHSLDVNVIQQ 200
                                                                                                                                                                                                                                                                                                                                                                                                8 EGLETVDNTLKGILE-----KLKVDLGVLQKSSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.9%; Score 83.5; DE Best Local Similarity 19.0%; Pred. No. 4.9; Matches 55; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08810712G Patent No. 6160106
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 13
                                                         Patentin Ver. 2.1
                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                   SOFTWARE: Pat
SEQ ID NO 4
LENGTH: 907
                                                                                                                                                                                                   US-09-546-238-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-810-712-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-810-712-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
```

```
1004 WDRTSGEEKHAGE-LINVLSDVNVTNGNAITCYHYTGMKVANTFSSKANRVENVTLE--K 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1110 SKIAHYQANRALVYKNIEKLLPFYN-----KSTIVKYGNLVKENSLLYQKELLSAVMM- 1162
131 ----H-----SPANIGECASDPTSISL----SLIDKHSQIIN 160
                                           791 ISPKLHVDKGFVNILMTSFLQYISSEVNPPSDETDSSSAPSKEQLEQEKQLLLSFKPVMQ 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 TSI----SLSLLDKHSQIINKFVNSVINTLKSTV-----SSLLQKEICPLIRIF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 WQLAKQKAQEAEKLLNNVISKLLPTNTDIF-----GLKISNSL-----ILDVKAEPID 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 83.5; DB 2; Length 1964; 24.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                             APPLICANT: Weiser, Jeffrey N. APPLICANT: Plaut, Andrew A APPLICANT: Plaut, Andrew TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: OF STREPTOCOCCUS PURUMONIAE INFECTION
                                                                                      161 KFVNSVINTLKSTVSSLLQKEI-C-----PLIRIFIHSLDVNVIQQ 200
                                                                                                              68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PANITCH SCHWERE JACOBS & NADEL, P.C. STREFT: 1601 Market Street, 36th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/790,912
FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 7600-401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                          Sequence 3, Application US/08790912
Patent No. 5976542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 IHS!?VNVIQQVVDNPQHKTQL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
TELEX: 831-404
INFORMATION FOR SEU ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1964 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 24.38
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leary, Kathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-790-912-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                    RESULT 11
US-08-790-912-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
δ
                                           g
                                                                                      ô
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
1077 WDRTSGEEKHAGE-LINVLSDVNVTNGNAITGYHYTGMKVANTFSSKANRVFNVTLE--K 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1134 DEVVSKESFEERGTMLDA----SQIVSKKAEINPLTLPTVE-----PLSTSGKKDSDF 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.9%; Score 83.5; DB 2; Length 2052; Sest Local Similarity 24.3%; Pred. No. 15; Adtches 49; Conservative 34; Mismatches 68; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 DGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 TSI----SLSLLDKHSQIINKFVNSVINTLKSTV-----SSLLQKEICPLIRIF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 WQLAKQKAQEAEKLLNNVISKLLPTNTDIF-----GLKISNSL-----ILDVKAEPID 84
                                                                                                                                                                                                       APPLICANT: Welser, Jeffrey N.
APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PANITCH SCHWAKZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/790,912
FILING DATE: 29-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                   Sequence 2, Application US/08790912
Patent No. 5976542
1236 ---KDDQVITDIVSNKQTANKL 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 IHSLDVNVIQQVVDNPQHKTQL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2052 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leary, Kathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-790-912-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inear
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-431-517F-2
                                                                                           RESULT 12
US-08-790-912-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
```

```
20.88;
                                        : 468 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 197 amino acids
TYPE: amino acid
                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sharp, Jeffrey S. REGISTRATION NUMBER: 31
    INFORMATION FOR SEQ ID NO:
                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicago
                                                                                                                              MOLECULE TYPE:
                                                                                   STRANDEDNESS
                                                                                                                                                                         NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-261-660A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                      US-09-004-838-121
                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ST'ATE:
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                       FEATURE:
                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                     . OTHER INFORMATION: No. 6265187e: human LBP-b DNA and amino acid sequence 0S-08-431-517F-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 DIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAG--PIIGQIINLKASLDL-LT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 EFHSLNIHSCELLHSALRPV-PGQGLSLSIS-DSSIRVQGRWKVRKSFFKLQGSFDVSVK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVTIETD-----PQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVIN----TLK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Indels 22; Gaps
                                                               APPLICANT: Scott, Randal W
APPLICANT: Marian N
ATITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS
FILE REFERENCE: 1103/113070503
                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 83; DB 4; Length 481;
18.5%; Pred. No. 2.1;
tive 42; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 STVSSLLQKEICPLIRIFIHSLDV------NVIQQVVDNPQHKTQL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Einhorn, Gregory P. REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/431,517F
CURRENT FILING DATE: 1995-05-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121, Application US/09004838 Patent No. 6350933 GENERAL INFORMATION:
Sequence 2, Application US/08431517F Patent No. 6265187 GENERAL INFORMATION:
                                                                                                                                                                                                               Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 18.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-004-838-121
                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE
                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

```
85 --- DGKGLNLSFPVTAN----VTVAGPIIGQIINLKASLD------LLTAVTIETDPQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SPLPNQGVNFKVLLTSRDVDVCTMMGVEANSILNMKILLDEEAQSLFMEFVQISSDVDPK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 THQ------PVAV-----LGECASOPTSISLSLLDKHSQIINKFVNSVINTLK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 LHKIGEDIVRKCCGLPIAIKTMALTLRNKSKDAWSDALSRLEHHD--LHNFVNEVFGISY 179
                                                                                                                                                                                                                                          90; Indels 55; Gaps
                                                                                                                                                                                                                                                                                                               31 LQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILD-----VKAEP1D- 84
                                                                                                                                                                                                                                                                                                                                                                                4 IQEAVADYLXIELKEKTKSARADMLRKMLVAKSD--GGKNKFLVILDDVWQFVDLEDIGL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Lipopolysaccharide Binding Protein Derivatives NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 STVSSLLQKEICPLIRIFIHSLDV------NVIQQVVDNPQHKTQLQTLI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 DYLODQETKYIFLLCGLFPEDYNIPPEELMRYGWGLNLFKKVYTIREARARLNTCI 235
                                                                                                                                                                  7.7%; Score 81.5; DB 4; Length 468; 20.8%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
LOCATION: 1..468
OTHER INFORMATION: /note- "RG2P deduced sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,660A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                              49; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27129/32137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y: United States of America
60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Theofan, Georgia
APPLICANT: Trown, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08261660A Patent No. 5731415 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-660A-51
```

Search completed: August 6, 2002, 16:53:54 Job time: 286 sec

| : ::|| : ::| | 170 SRICEMIQKSVSSDLQPYLQTLPV 193

us-10-020-139-1.rge

```
M8320 Rattus norv
M26806 Mouse parot
AE001965 Deinococc
AF423315 Homo sapi
E53840 LUNX gene a
AF172993 Homo sapi
E53841 LUNX gene a
AB024937 Homo sapi
BC012549 Homo sapi
AF158745 Homo sapi
                                                                                                                                                                                                                                                                                       M26807 Mouse parot
b43949 Human mRNA
AX123429 Sequence
AX066081 Sequence
AC107180 Rattus no
AL139090 Human DNA
AC021774 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX224643 Sequence
AX224643 Sequence
BC008429 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACO98322 Rattus no
D88464 Rainbow tro
ACO95073 Rattus no
ACO94951 Rattus no
ACI07726 Mus muscu
                             U79413 Bos taurus
U79414 Bos taurus
BC010288 Mus muscu
                                                                                                         M83209 Rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Streptomy
Homo sapi
Macaca fa
Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapi
Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1058)
                                                                                          X01697 Mouse mRNA
                                                                                                                       X68699 M.musculus
AX061621 Sequence
AF432917 Homo sapi
                                                                          AL121901 Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dumas milne Edwards, J.B., Bouqueleret, L. and Johert. S. Complementary dna's encoding proteins with signal peptides Patent: WO 0100806-A 26 04-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                               AX127153
AL445327
AC005411
AB056750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX301908 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP001497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX301906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67. .816
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           BTU79414
BC010288
HSBA49G10
                                                                                                                                                      MUSPSPA2
AE001965
                                                                                                                                                                                                  E53840
AF172993
                                                                                                                                                                                                                             E53841
AB024937
BC012549
AF158745
                                                                                                                                                                                                                                                                                         MUSPSPA3
                                                                                                                                                                                                                                                                                                                      AX123429
AX066081
AC107180
                                                                                                                                                                                                                                                                                                                                                                  AL139090
AC021774
AX127153
SC8A2
AC005411
AB056750
AC007391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP001304
AX301906
AX301908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX224647
AC098322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX092346
AX224643
                                                                                                                                       RATSMGB
                                                                                          MMPSPR
RATPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1058
                                                                                                                         MMPSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX061621.1 GI:12406703
                                                                                                                                                                                                                                                                                           10
                                                          100
                                                                                                                                                                                                                1011
1015
1015
10053
1084
227
3186
837
53792
                                                                                                                                                                                                                                                                                                         3.8 3186
3.8 950
3.8 15392
3.8 167366
3.8 167366
3.7 163903
3.7 207767
3.7 207767
3.6 1684
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.6 1636
3.
                                                                                                                         13962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FR)
                             223.1
119.3
118.6
16.8
6.9
6.3
6.1
4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                              1019.8
746.8
213.4
219.4
199.4
199.6
173.2
70.6
65.2
65.2
65.6
42.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              മാമായ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.
36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
AX061621
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                         Clarins 1 d : 2
                                                                                                    August 6, 2002, 16:01:08; Search time 1816.11 Seconds (without alignments) 11845.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                1 CACGAGATTTCATGAGCATC......AAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                         1797656 segs, 10463268293 residues
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_htg_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_un:*
em_vi:*
em_htg_hum:*
em_htg_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_htgo_inv:*
                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                 US-10-020-139-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9b_btg.*
9b_on.*
9b_on.*
9b_on.*
9b_pt.*
9b_pt.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_or:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_pat:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qb_vi:*
em_ba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      en_mu:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_om:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              еп_го:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           GenEmb1:*
                                                                                                                                                                                     1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                     Title:
```

```
/translation="MLQLWKULLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
ETVDNTLKGILEKLKVDLGVLQKSSAMOLAKQKAQBARKLLNNVISKLLPTNTDIFGL
KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIGQIINLKASLDLLTAVTIET
DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRTFIHSLDVNVIQQVVDNPQHKTQLQTL"
                                                                                                                                                                                                                                                 ö
                                                                                                         /note="Von Heijne matrix score 5.20 seq QLWKLVLLCGVLT/GT"
                                                                                                                                                                                                                                                                                                                   66 ACTIGITCICCIGIGGGGGGGGGGCTCACTGGGACCTCAGAGTCICTTGACAAICTIGG 125
                                                                                                                                                                                                                                                                                                                                   126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                   144 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 203
                                                                                                                                                                                                                                                                                                                                                                                                                               186 AGTIGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                              246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 CAATGICATITCIAAGCIGCITCCAACIAACAGGGACAÍTITITGGGIIGAAAATCAGCAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 CTICCCTGICACGGGAAIGICACIGIGGCCGGGCCCAICATIGGCCAGAIIAICAACCI 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GATITCATGAGCATCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                            546 GCCIGITGCCGTCCTGGGAGAAIGCGCCAGTGACCCAACCAGCAICTCACTITCCIIGCT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       606 GGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 CACTGTATCCTCCCTGCTGCAGAAGAGATATGTCCACTGATCCGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684 CACTGTATCCTCCCTGCTGCAGAGAGATATGTCCACTGATCCGCATCTTCATCCACTC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 CCTCGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%; Score 1019.8; DB 6; Length 1058; 99.8%; Pred. No. 4.4e-267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                             4.4e-267;
                                                                                                                                                        234 t
                                                                                                                                                                                                                                      0; Mismatches
/protein_id="CAC24982.1"
/db_xref-"G1:12406704"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 9
                                                                                                                        1023. .1028
                                                                                                                                          .1058
                                                                                                                                                     302 c
                                                                                                                                                                                                                                   Matches 1021; Conservative
                                                                                                                                      1042.
                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                  291 a
                                                                                                                       polyA_signal
                                                                                             sig_peptide
                                                                                                                                      PolyA_site
COUNT
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
PRI 07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Cranslation-"MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
ETVDNTLKGILEKLVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGL
KISNSLILDVRAEPIDDGKGTMLSPYTANVTVAGPTIGQIINLKASLDLLTAVTIEF
DPQTHQPVAVLRECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRIFHSLDVNVIQQVVDNPQHKTQLQTLI

210 c 163 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata: Vertebrata, Euteleostomi; Mammalia: Eutheria; Primates: Catarrhini; Hominidae; Homo. (backatesh. 20)
Venkatesh. 3.G. Geetha, C. and Gorr, S.-U.
A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland
                                                                                                                                                                            966 CAGAACAGGAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                                                                                                                                                                             804 AACCCTCATCTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 863
                                  846 AGIGGCITGCCCCACCCCTTATAGCAICTCCCTCCAGGAAGCTGCTGCCACCACCTAAC 905
                                                       49 ATGCTICAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTCACTGGGACCTCAGAGTCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 CTICTIGACAATCITGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular and Craniofacial
501 S. Preston Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906 CAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="salivary protein; putative BPI protein; PSP; similar to BSP30 and plunc/lunx"
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens parotid secretory protein mRNA, complete cds. AF432917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.6%; Score 746.8; DB 9; Length 750; 99.7%; Pred. No. 1.2e-192; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="parotid secretory protein"
                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-OCT-2001) Molecular,
Biology, University of Louisville,
Louisville, XY 40292, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism "Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAL28113.1"
/db_xref="G1:16755850"
                                                                                                                                                                                                                                                                                                                                                                                   750 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="parotid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 750)
Venkatesh, S.G. and Gorr, S.-U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                 AF432917.1 GI:16755849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start+1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              AF432917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 a
                                                                                                                                                                                                                                                  1026 AAA 1028
                                                                                                                                                                                                                                                                                    1044 AAA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                       AF432917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                  ò
                                                                    qq
                                                                                                      δ
                                                                                                                                      οp
                                                                                                                                                                            ó
                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      СP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
Bru79413 999 bp mkNA linear MAM 09-DEC-1996
Bos taurus common salivary protein BSP30 mkNA, form a, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
The clouds and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-NOV-1996) Dairy Science Group, AgResearch, Private
121 CACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTC 180
                                                                                                                                              300
                                                                                                                                                                                                                                                                   408
                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                            528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 ATCTCACTITCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 709 GGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGAGGGACTTCAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTC
                                                                                                                                                                                                 GCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTT
                                                                                                                                                                                                                GGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGATTATCAACTGAAAGCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 ATCTCACTTTCCTTGCTGGACAAACACGGCAAATCATCAACAAGTTCGTGAATAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATC
                                                                                                                         GACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAA
                                                                                                                                                                                                                                                                     349 GGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATGATGATGGC
                                                                                                                                                                                                                                                                                                     AAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 999)
Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        769 CACAAAACCCAGCTGCAAACCCTCATTTGA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bag, Hamilton, New Zealand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U79413
U79413.1 GI:1710366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                           409
                                                                                                                                                                                                                                                                                                                                                                                                                 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BTU79413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                   pp
                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  аa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                          g
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                           ò
```

```
/product.d="AAB38282.1"
//prodecin_d="AAB38282.1"
//db_xref="G1:1710367"
//db_xref="G1:1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 AGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGGAGGAGGCC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AGACTGAATT----------GGAATCCAGGTGTTTGAACGATGTTGTGGAGGAGACCC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 AGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 ATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGGAATGTCACTGTGGCCGGGCCCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 TCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 TGTTGGGTGAGATTGTCAAACTGGACCTCAATGTGGACCTCCAAACTAGTGTCAGCATTG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 AAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCAA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 CCAGCATCTCACTTTCCTTGCTGGACAAACACAGCGAAATCATCAACAAGTTCGTGAATA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 GCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCAC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     607 TTGGAGTCAACCTTGTAAGACAGTTGGTGTCCTCTGTAGTGCAGCACGAGCTGTGCCCAC 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704 TGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AATCTCTTCATCATTCGTGGCAA-----CGATGTTCTGAGGAGGCTGATATCTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 TICTICACGAGGGACTIGAGACAGTIGACAATACTCTTAAAGGCATCCTIGAGAAACTGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 TTACAGGGGTGAGAATCAGGAACGTCCAGGTCCCGGATATCACATTCGAAGCGA---CTT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 GAATCCGTGAACTCCTTGAAAGCCTGGATACAGAGTGTATTAAGAAACTCATTGGTGAAC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 AAAGCATCTCACTCACGGTGCTGCACAGGCGCCCTGGACTGCTCAACGATGTTGTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ACAAGATGGTTCAGCTTTGGAAACTTGTTCTCTTGTGCGGCCTGCTCGCTGGGACCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%; Score 237.4; DB 4; Length 999; 57.3%; Pred. No. 9.8e-54; tive 0; Mismatches 386; Indels 35.
                                                                                                                                                                          /note≃"common salivary protein, form a"
                                                                         /tissue_type="parotid gland"
36. .767
/organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                             /product="BSP30"
                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 57.39
Matches 564; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
MAM 09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSTIELLFONLKTELESRCSDEVVEQOETENFLEQLISRIFOVVSRLTGVRIRWOVP
TTFEATENSMANULPITADVTVSLPFLGEIVDLDLAVDLOJTVSLETDTEDPQVVV
GECTNNPESISLTVLHSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDA
ECVEKLIGESQDTTQQEPEGSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVQLWKLVLLCGLLAGTSASI,PDIRGNDVLRKLKSGLERGLDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bo. 1 (bases 1 to 1024)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haigh, B.J., Wilkins, R.J. and Wheeler, T.T. The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1024)
Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
Direct Submission
Submitted (21-NOV-1996) Dairy Science Group, AgResearch, Private
                                                                                                                                                                944 AGATACCCCTTCTCCTCACAGTCAGAACAGCCTCTACACATGTTGTCCTGCCCTGG 1003
                                                                                                                                                                                                                                                                                                                                                                                                    BTU79414 1024 bp mRNA linear MAM 09-DEC-1
Bos taurus common salivary protein BSP30 mRNA, form b, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
787 GCCTGCTGACTGGTTCCAGGACGTGACTGAATCTCTGTACCGTCT---TCCTCTGGGACG 843
                                                                                  884 GAAGCTGCTGCCACCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACAGAAGGACTTCCC 943
                                                                                                           904 A-----CACTCGTCGTCACAGTCAGGA---CACCCTATGCTTGTCACCCTCCACCCAG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 AAAAGAIGCIICAGCIIIGGAAACIIGIICICCIGIGCGGCGIGCICCICACIGGGACCICAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AGTOTOTOTOTOGAATOTOGCAATGACCTAAGCAATGTOGTGGATAAGCTGGAACOTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note*"common salivary protein, form b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.3%; Score 219.4; DB 4; 56.9%; Pred. No. 7.9e-49; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="parotid gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAB38283.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism~"Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="G1:1710369"
                                                                                                                                                                                                                                                   1004 CAATAAAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                         956 CAATAAAGAGCCTTTTCAGCAAAA 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bag, Hamilton, New Zealand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="BSP30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          U79414
U79414.1 GI:1710368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                BTU79414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                           BTU79414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITCE
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                      Q
                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                         g
                                                                                  ô
                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
```

```
974 bp mRNA linear ROD 29-OCT-2001
IMAGE:2616413, mRNA, complete cds.
BC010288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                     164 ITCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGA 223
                                                                                    224 AGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAGGCCC 283
                                                                                                                                                                           284 AGGAAGCIGAGAAATIGCIGAACAAIGICAITICIAAGCIGCIICCAACIAACACGGACA 343
                                                                                                                                                                                                                   246 AGGAAACTGAGAATTTCTTGGAACAACTCATTTCTAGAATTTTTCAAGTAGTGAGCAGGC 305
                                                                                                                                                                                                                                                                306 TTACAGGGGTGAGAATCAGGAACGTCCAGGTCCCGGATATCACATTCGAAGCGA---CTT 362
                                                                                                                                                                                                                                                                                                                                                     404 ATGCCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGCAATGTCACTGTGGCCGGGCCCA 463
                                                                                                                                                                                                                                                                                                                                                                                 537 AAAGCATCTCACTCACGGTGCTGCACACTTTGACTCGTCAACGATGTCGTGGACA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                       464 TCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 AAACTGATACTGAAGACCCCCAG-----GTGGTCGTGGGAGAATGCACCAACAACCCAG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 CCAGCATCTCACTTTCCTTGCTGGACAAACACCGCAAATCATCAACAAGTTCGTGAATA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 GCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCAC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 TTGGAGTCAACCTTGCGAGAAGGGTGGTGTCTCTGTAGTGGAGGGCGAGCTGTGCCCAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 TGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       657 GATICCGCGAGCICCTIGAAAGCCIGGAIGCAGAGIGTIGAGAAACICAIIGGCGAGI 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764 CTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAG----- 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         717 CTCAGGACACCACCAACAGGAACCTGAAGGCAGCAGATGAGGAAACCGCTGGGATGCCC 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 GACCACTGTGGTGCTGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCTTATAGCATCT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                777 GCCTGCTGGGTCTCTTTCCAGATTGGTTCCAGGACTAGACTGAATCTCTGTACCGTCTCC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             876 CCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     837 CTCTGGGACAGGCGGTGCTGCCACCATCCCCCAGGAATGACAACTGAGCCCAGTCAAAGG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 936 ACCTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACACATGTTGTCCT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897 ACACTCTCGGATACTCATGCTC -- -- ATAGTCAGGACACCCTATGCTCATCACCTCC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524 AAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCCAGTGACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996 GCCCTGGCAATAAAGGCCCATTTCTGCAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC010288.1 GI:16307480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC010288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                        a
                                                                                  õ
                                                                                                                            q
                                                                                                                                                                           ò
                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                             P
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

S

```
g
                                                                    qq
                                                                                                                                                                      q
                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 16 Row: g Column: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month oid virgin mouse." /clone_lib="NCI_CGAP_Mam6" /lab_nost="DHIOS" /lab_nost="DHIOS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLIDYELLQQATSWPAKNSILETUNTADLGNEKSFTSLNGLLKINNLKYLDFQAK
LSSNGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGK
CSSNTDKISISLLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MFQLGSLVVLCGLLIGNSESLLGELGSAVNNLKILNPPSEAVPQ
                                                                                                                                                                                                                                                                                                                                                     Sequencing Center
Center code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Web Site: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
Villalon, D.K., Luna, Helford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                 Direct Submission
Submitted (05-JUL-2001) National Institutes of Health, Mammalian
                                                                                               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AITCIAGAAACGTIGAACACAGCGGACCTTGGCAATTIAAAAAAGCTIIACAICI---TTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 360; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGGGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Jeffrey Green M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I. M.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="parotid secretory protein"
                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 198; DB 10;
Pred. No. 5.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:11605 IMAGE:2616413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAH10288.1"
/db_xref="G1:16307481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="LocusID:19194"
/db_xref="taxon:10090"
                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOGILISNILAGOVQLAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                       Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%;
55.7%;
1 (bases 1 to 974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 55.7
Matches 511; Conservative
                           Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                 TITLE
JOURNAL
  REFERENCE
                           AUTHORS
                                                                                                                                                                                 REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
HSBA49G10
Human DNA sequence from clone RPI1-49G10 on chromosome 20 Contains a gene similar to bovine salivary protein BSP30,the LOC51297 gene for LUNX protein, 5, end of a gene encoding a protein similar to pseudogene similar to salivary gland protein, a novel gene, a pseudogene similar to STAT-induced STAT inhibitor-2, a pseudogene similar to ribosomal protein L12, a putative novel transcript, AL121901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jun 5, 2000 this sequence version replaced gi:8017404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 CCATIGCTICAGTACGICCTCAGCACACIGAAICCAAGIGTICIICAGGGICTCCTCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 AATCTACTG --- GCAGGACAGGTACAACTTGCCCTCTGAAGAGGAAGAACAGAAGGATGC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              774 CACAACTCTCCTGCTGCTACTCTCCAGTGGTTTCATCTTACTTCTGATGGCATTTCCCT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 CCAGGAAGCTGCTGCCACCACCTAACCAGGGTGAAAGCCTGAGTCCCACCAGCAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       834 CTAGAAAG----TGCTACTATCATCCACATTTCTACCTGAG-ACCACCAAAGGACCC 888
340 GACATITITIGGGTIGAAAATCAGCAACTCCCTCATCCTGGAIGTCAAAGCTGAACCGATC 399
                                                                            297 AATGGTTTATTGTTGAAAATCAATAATGTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 356
                                                                                                                                                     400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                             357 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 416
                                                                                                                                                                                                                                                                                                          460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                   417 certrearregeaagaeggregaearricestrectregaecrearaaarreacrere 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 ATTAAAACCAAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; BSP30; CpG island; LOC51297; LUNX; RPL12; STAT-inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAAATGCGCCAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 GATGGTGTCTCTACCCTCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTCCTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL121901.20 GI:8249854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Pr
1 (bases 1 to 161593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    940 TCCCAGATACCCCTTCTC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889 TCCCAAATICTCTTCTC 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracey, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSBA49G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ø

```
join(36522. .36678,40308. .40452,41455. .41562,42783. .42935,
45523. .45604,46980. .47043,47896. .47936)
/gene="bA49G10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id-"CaC03546.1"
/db_xref-"G1:9801234"
/translation-"MLQLMKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
/translation-"MLQLMKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
/translation-"MLQLMSSAMQLAKQKAQEAEKLLNNVISKLLPTNTDIFGL
KISNSLILDVKAEFIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPQTHQPVAVLGECASDPTSISLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31882. 32061

/note="3 copies 60 mer 73% conserved"

/note="5 copies 2 mer ct 63% conserved"

31921. 32032

/note="MER47 repeat: matches 2251. 2322 of consensus"

33733. 33785

/note="MER47 repeat: matches 1. .55 of consensus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence-not_experimental
/product-"ba49G10.1 (similar to bovine salivary protein
BSP30)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="bA49G10.1 (similar to bovine salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1PA8 repeat: matches 4514. 5125 of consensus" 38750. 39785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note⇒"L1PA8 repeat: matches 5128. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: cDNas: Em:U79414 Em:U79413 Em:AX061621 match: ESTs: Em:A1654622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: proteins: Tr:P79125 Sw:P07743"
/codon_start=1
                                                                                                                                                                                                     71031. 21263
7note="match: GSS: Em:AZ055779 Em:AZ084220"
21144. 21225
                                                                                                                                                                                                                                                                                                 /note="41 copies 2 mer ag 75% conserved"
complement(21172. .21428)
/note="match: GSS: Em:A035327"
/note="match: GSS: Em:A0727877"
                                                                                                                                                                         /note="4 copies 60 mer 69% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AQ152593"
23955. .24456
/note="match: GSS: Em:AQ508832"
26979. .27422
/note="match: GSS: Em:AQ636646"
31882. .32061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ897745"
/note="match: GSS: Em:AQ897745"
                                                    /note="match: GSS: Em:AZ102442"
/note="match: GSS: Em:AZ102442"
/note="match: GSS: Em:AZ102442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18333. .18770
/note="match: GSS: Em:AQ765930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AQ429347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: STS: Em:G31731"
53842. .53969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental complement(53831 54131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35535. .48787
/gene="bA49G10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="bA49G10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bA49G10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="bA49G10.1"
                                                                             complement (20975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMEL: Swi. SWISSPROT: Tr.; TREMBL: Wp.; WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP11-49G10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP1-1874 is at 1 in this sequence. The true left end of clone RP5-11874 is at 164.94 in this sequence. The true right end of clone RP4-733023 is at 27823 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequence with a alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPII-87400 is from the library RPCI-11.1 constructed by the group of pieter de Jong. Por further details see

Http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: STS: Em:HS922114S" //note="match: STS: Em:HS922114S" //note="madem repeat. Forced join. Approximately 500 bases missing according to restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5140. .5183
/note="22 copies 2 mer tt 75% conserved"
5184. .5344
/note="LIPA2 repeat: matches 5986. .6146 of consensus"
complement(6104. .6463)
/note="match: GSS: Em:AQ339300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3030. .3174 /
/nole-"L1PB3 repeat: matches 5941. .6084 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530. .603
/note="37 copies 2 mer ca 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anote-"33 copies 2 mer ca 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6120. .6239
//note="2 copies 60 mer 85% conserved"
complement(8476. .902)
//note="match: GSS: Em:Ap537190"
complement(14766. .15061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copies 77 mer 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1. .107)
/note="match: GSS: Em:AQ607627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ051854"
137. .548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ550113"
530, .603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:AQ458133"
18328. .18828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AL001671"
16225. .16387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AL013146"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18328. .18828
/note="match: GSS: Em:AQ532957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="20"
/clone="RP11-49G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233. .686
/note≃"2 c∩
613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .161593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

5;

```
/product="put. PSP (parotid secretory protein).(aa 1-215)"
227 c 168 g 252 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 AAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCAAATTGAAACT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 GGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCCATTAAAACC 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 GATCCCCAGACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 ATCTCACTITCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              649 ATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCACTGATC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 CGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622 CAGTACGTCCTCAGCACAGAGTCCAAGTGTTCTTCAGGGTCTCCTCTCTAATCTACTG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        769 CACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTG 828
                                                                                                                                                                                                                                                                                                                       18.5%; Score 190.6; DB 10; Length 867;
55.3%; Pred. No. 5.6e-41;
Live 0; Mismatches 359; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               49 ATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 CTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 CACGAGGGACTIGAGACAGITGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGIC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGCATTCTAGAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 ACGITGAACACAGCGGACCITGGCAATITAAAAAGCTITACAICTITGAATGGTTAIT- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 TCTACCCTCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTCCTATGTCCATTGCTT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGTTCCAACTTGGAAGCCTTGTTGTTGTGTGGCCTGCTCATTGGGAACTCAGAGTCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CTTCTTGGTGAACTTGGCAGCGCTGTGAATATTTGA--------
                                             /protein_id="CAA25846.1"
/db_xref="GI:758163"
                                                                                                                                                                                   LOGLLSNLLAGOVQLAL"
61. .705
              /codon_start*1
/product*"PSP"
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.33
Matches 503; Conservative
                                                                                                                                                                                                                                                 220 a
                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469
CDS
                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΔD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οp
                                                                                                                                                                                                                                                                                                                                                                                                       ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROD 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musilaes 1 to 867)
1 (bases 1 to 867)
Madsen, H.O. and Hjorth, J.P.
Molecular cloning of mouse PSP mRNA
Nucleic Acids Res. 13 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                match: proteins: Tr:095102 Tr:088582 Tr:014542 Tr:014509
Tr:062225 Tr:015097 Tr:035718 Tr:090x77 Tr:090x78
Tr:070512 Tr:035960 Tr:09PW70 Tr:09Y5R1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48582 CCCTTGGTCTCATTCCAGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCC 48641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818 CCACTGTGGTGCATGCTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   878 CICCAGGAAGCTGCCACCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGAC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             938 CITCCCAGAIACCCCTICTCCTCACAGICAGAACAGCAGCCICTACACATGITGICCTGC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 191; DB 9; Length 161593;
Pred. No. 6.8e-41;
0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse mRNA fragment for parotid secretory protein (PSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="bA49G10.2"
/note="bA49G10.2 (similar to STAT-induced STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parotid secretory protein; signal peptide.
                /note="match: GSS: Em:AQ533658"
54030. .54138
                                                                                                                         /note="match: GSS: Em:AQ378081"
53970, .54139
                                                                                                                                                                                     53972. 54142
7note="match: GSS: Em:AQ429347"
54000. 54141
                                                                                                                                                                                                                                                 Em: AQ392510"
54139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                              Em: AQ415287"
                                                                                                                                                                  /note="match: GSS: Em:AQ527291"
                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AG000935"
54041, .54149
                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ392891"
.54141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%; Score 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48762 CCCTGGCAATAAAGGCCCATTTCTGCA 48788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 CCCTGGCAATAAAGGCCCATTTCTGCA 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                            /note="match: GSS:
53958. .54139
                                                                                                                                                                                                                                               /note="match: GSS:
complement(54027...
                                                                                                                                                                                                                                                                                                                                                                                         /gene="bA49G10.2"
54767, SEKE
  complement (53844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                     55668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X01697
X01697.1 GI:53810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 95.2%
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                               54041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              louse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMPSPR
                                             misc_feature
                                                                                                                                                          misc_feature
                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMPSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
```

qq

ó

qq

ò

οy

qq

ô

œ

```
/translation="MFQLGSLVVLCGLLIGTSESLLCDVANAVNLDILNSPSEAVAQ
NNLDVGSQCQQATTWPSAKDSILETLNKVELCONSOFFPLUGLLRVNKFFVLDLQAG
LSSNGKDIDLKLPPLFEISTSLPV1GPTLDVAVSLDLLNSVSVQTNAQTGLFGVTLGR
CSGNTDKISISLLGRRLPFVNRILDGVSGLLTGAVSILLQNILCPPLQYLLSTNSGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretroy protein are alternatively regulated members of a salivary protein multigene family J. Biol. Chem. 267,\ 2679-2687\ (1992)
                                                                                                                                                                                                                                                                                                                         RATPSP 962 bp mRNA linear ROD 24-MAR-1998 Rattus norvegicus neonatal submandibular gland protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="neonatal submandibular gland protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-APR-1993) Molecular and Cell Biology, University c
California, 401 Barker Hall #3204, Berkeley, CA 94720-3204, USA
                                                                                                          739 CCTGCTGGCTACTCTCCAGTGGTTTCATCTTACTTCTGATGCCATTTCCCTCTAGAAAG- 797
                                                                                     889 TGCTGCCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mirels,L., Miranda,A.J. and Ball,W.D.
Characterization of the rat sallvary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mirels, L. and Ball, W.D. Neonatal rat submandibular gland protein SMG-A and parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="neonatal submandibular gland protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="proacinar"
/Lissue_type="submandibular gland"
/dev_stage="neonatal"
1..962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 330 (Pt 1), 437-444 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC06334.1"
/db_xref="G1:206457"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley'
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="psp"
/note="secreted form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQGLLSNVLTGQLAVPL"
                                                                                                                                                                                                                                                                                                                                                                        psp) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /deue="bsp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dene="psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="psp"
107. .751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /deue="psp"
                                                                                                                                                                                                                                                                                                                                                                                                             M83209.1 GI:206456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                          949 CCCCTTCTC 957
                                                                                                                                                                                                                    854 CTCTTCCTC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98129760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92129360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mirels, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                                                                                                                                                          M83209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PolyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                       RATPSP
                                                                                                                              QΩ
                                                                                                                                                                          ò
                                                                                                                                                                                                                    qq
                                              qq
                                                                                       ð
```

```
180 ATCTGAATCTGGATGTGGGGGTCACTTCAGCAAGCCAACTTGGCCATCAGCCAAGACA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 TCGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 CTTCCAATGGCAAGGACATGGACTGAAACTGCCCCTGGTTTTTGAAATTTCTTTTTCT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 GCCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 TGCCTGTCATTGGCCCTACGCTCGACGTTGCTGTTTCCTTGGACCTCCTAAACTCAGTCA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 CAATTGAAACFGATCCCCAGACACACAGCTGTTGCCGTCCTGGGAGAATGCGCCAGTG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578 ACCCAACCAGCATCTCACTTTCCTTGCTGGACAACACACCAAATCATCAACAGTTCG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 TGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGGAGGAGTAT 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 IGGATGGIGTATCTGGCCTCCTCACAGGTGCAGTGTCAATCCTGCTGCAAACATCCTAT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 GYCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCG 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 GCCCAGTGCTCCAGTACCTCGTCAGCACAATGAGTGGAAGTGCTATTCAGGGTCTCCTCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     758 ATAATCCTC-AGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGG 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       717 CTAATGTACTAACAGGACAGCTAGCAGTCCCTCTCTGAAGAGGAAGAACAGAAGGAGGAGAA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     817 ACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCCACCCCCTTATAGCATCTC 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        777 GCCATGACCACCCCTGCTGGTTAGTCTCCACTGGCTTTATTTTACTTCCGGTGGCATTTC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877 CCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGA 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   837 TTTCTGGGAAG --- TTCTACTATCATCCACACAAAGTCTACCTGATACCAACGGAAGGA 892
                                                                                                                                                                                                                                                                                                                                                       96 CCTCAGAATCACTTCTTGGTGACGTTGCCAATGCTGAATAATTTG-------142
                                                                                                                                                                                                                                                                                                                                                                                                    58 AACCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ------GACATTCTTAATTCTCCTCTGAAGCTGTCGCTCTAGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 AACTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 AGGCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 GCATTCTTGAAACATTGAACAAAGTGGAGCTTGGCAATTCAAATGGCTTTACACCT--T 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 CGGACATTTTTGGGTTGAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGA 397
                                                                                                                                                                                                                                                                                                    98 CCTCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGG 157
                                                                                                                                                                                                                              36 CCAAACCAAAGATGTTCCAACTTGGGAGCCTTGTGGTCTTGTGGTGGCCTGCTTATTGGGA 95
                                                                                                                                                                                                 38 CAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGA 97
                                                                                                   DB 10; Length 962;
                                                                                                                                                0; Mismatches 388; Indels
                                                                                                                     3.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 173.2;
53.1%; Pred. No. 3.1e
199 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         937 CCTTCCCAGATACCCCTTCTCC 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      893 CTTTCCCAGATTCCCTTCTTC 914
  O
                                                                                                                                                   Matches 490; Conservative
                                                                                                                                                                                                                                                                                                                               257
                                                                                                                           Best Local Similarity
  ø
                                                                                                   Query Match
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Mirels, L. and Ball M.D. Bronein SMG-A and parotid ret submandibular gland protein SMG-A and parotid secretroy protein are atternatively regulated members of a salivary protein multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROD 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-APR-1993) Molecular and Cell Biology, University of California, 410 Barker Hall #3204, Berkeley, CA 94720-3204, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7696 GTGACTCTTGTTTCTGCAGGCCTTTCATTGGCAAGACGGTCGACATTCTGTTTCCTTG 7755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7756 GACCTCATAAATTCACTCTCCATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACC 7815
                                                                                                                                                                                                                                                                                                                                                                                               439 GCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 GACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACCAGCCTGTTGCCGTC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 CTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATSMGB 827 bp mRNA linear ROD 07-API Rattus norvegicus neonatal submandibular gland proacinar cell protein precursor (SMGB1/SMGB2) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mirels,L., Miranda,A.J. and Ball,W.D. Characterization of the rat salivary-gland B1-immunoreactive
                                                                                                                                                                                                                                                                                                               6.9%; Score 70.6; DB 10; Length 13962; 60.8%; Pred. No. 3.7e-08; Live 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                      3 others
                /product="parotid secretory protein"
11287. .11361
/gene="Psp"
                                                                                                                                                                                                               /product="parotid secretory protein" 3075 c 3231 g 3930 t 3 o
                                                                                                               /product="parotid secretory protein"
12262, .12433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 330 (Pt 1), 437-444 (1998) 98129760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem. 267, 2679-2687 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                    3231 g
                                                                                                                                                                         /note="exon i"
                                                                       /note="exon h"
                                                                                                                                                    /gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M83210.1 GI:206989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 827)
                                                                                                /number~8
                                                                                                                                                                                              /number=9
/number-7
                                                                                                                                                                                                                                                                                                                                                         Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7876 TTATTCATC 7884
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619 CAAATCATC 627
                                                                                                                                                                                                                                    3723 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92129360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mirels, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATSMGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                     ROD 29-OCT-1999
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                            l (bases 1 to 13962).
Svendsen, P., Laursen, J., Krogh-Pedersen, H. and Hjorth, J.P.
Novel salivary gland specific binding elements located in the PSP proximal enhancer core
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-OCT-1992) T.R. Mikkelsen, Department of Molecular
Biology, University of Aarhus, CF Mollers Alle 130, 8000 Aarhus,
DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Lambda-PHAGE (Lambda L47.1)"
/clone="Lambda YP1, Lambda YP3, Lambda YP7"
/map="Estimate: 69 cM from centromere"
/note="Allele: b"
                                       linear
                         MMPSPG 13962 bp DNA linear M.musculus Psp gene for parctid secretory protein. X68699
                                                                                                                                                                                                                                                                                      Nucleic acids research. 26 (11), 2761-2770 (1998) 98256451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
/product="parotid secretory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="parotid secretory protein"
7716. .7868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product "parotid secretary protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="parotid secretory protein"
10779. .10842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="parotid secretory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="parotid secretory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain-"C3H/As"
/db_xref="taxon:10090"

    1578
    evidence-experimental

                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                          X68699.1 GI:53809
parotid secretory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="exon c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"exon b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon d"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="exon e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="exon f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10043. .10124
/gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="exon g"
                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 13962)
Mikkelsen, T.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .12433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dene-"Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6133. .6274
/gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5480. .5608
/qene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /deue="bsb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /deue="Psb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Psp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .13962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=5
                                                                                                                                                          Mus musculus
                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                    9592166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                        DEFINITION
                                                                         ACCESSION
VERSION
KEYWORDS
                                                                                                                                                        ORGANISM
                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                      PUBMED
                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                       TITLE
  RESULT
                                                                                                                                      SOURCE
                    MMPSPC
```

```
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE001965.1
                                                                                                                                                                      87004556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE001965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                      intron
         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE001965/c
                                                               REFERENCE
                                                                               AUTHORS
                                                                                                                                                                        MEDLINE
                                                                                                                                                       JOURNAL,
                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCUS
                                                                                                                                                                                                                                                    /traislation="MPOLGSLVVLCGLLIGTSGSLFDIFQNPELDVESVWSEINYRIR
YAEFWALDMADYLSKRGTBEKIRDELIAUNHEVSBYGDBYTLKRPMALMASLSLP
AHDIJTDVSISMEATTSFATEKDPKTGRRVLNMQRCSLNTDNTSISLLNRKSNFVNLA
LDSALYLIKRGLTLPVRRQLCPVLQLIISNTFHPDETSNPQTAISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse parotid secretory protein (PSP) gene, exon 2, clone YPLE2.8. M26806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 TCGAGITGAAAATCAAGGACCTCAGAATTCTGAACCTGAATCATGAAGTGTCTCCCAATG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 GIGATITAACTACTGATGICTCTATTCTATGGAGGCAATAACTTCCTTTGCTATTGAAA 394
                                                                                                                                                                                /product-"neonatal submandibular gland proacinar cell
                                                                                                                                                                                                                                                                                                                                                                                                                   /product="neonatal submandibular gland proacinar cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 GCAAAGGCCTTAACCTGAGCTTCCCTGTCACGGGAATGTCACTGTGGCCGGGCCCATCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 ITGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 CTGATCCCCAGACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 AAGATCCCAAGACTGGCGTCGTGTCCTGAACATGCAGCGATGCTCACTTAATACAGACA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 GIGATGAAGITACCCIGAAGAIGCCCAIGGCICITAAIGCAICTCTGTCTGCCIGCCC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 ATACCTCCATTAGCTTGTTGAACAGAAAAGTAACTTTGTCAACTTAGCTCTGGACTCTG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   647 IGAICAACACGCIGAAAAGCACIGIAICCICCCIGCIGCAGAAGGAGAIAIGICCACIGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                          /note-"parotid gland protein SMGB; sublingual gland protein SMGB; differently N-glycosylated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 GCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%; Score 65.2; DB 10; Length 827; ilarity 48.4%; Pred. No. 8.7e-07; Conservative 0; Mismatches 193; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parotid secretory protein; secretory protein. 2 of 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (strain C3H.Amy-YBR) spleen DNA.
/Lissue_type="submandibular gland"
/dev_stage="neonatal"
1. .827
                                                                                                                                                                                                 protein precursor"
/protein_id="AAC12783.1"
/db_xref="G1:206990"
                                                                                                                                                                                                                                                                                                                                                                                               /note="secreted protein"
                                                                                           /qene="SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /yene="SMGB1/SMGB2"
206 c 160 q
                                                        "SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                               "SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                /gene="SMGB1/SMGB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 g
                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M26806.1 GI:200555
                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .816
                                                                                                                                                                                                                                                                                                                                                                .642
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
811. .81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707 TCCGCATCTTCATC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5:5 TCCAATTAATCATC 588
                                                                                                                                                                                                                                                                                                                                               /gene-
85. .64
                                                          /dene*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSPSPA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ωp
```

```
Poulsen.K., Jakobsen.B.K., Mikkelsen,B.M., Harmark,K., Nielsen,J.T. and Hjorth,J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcaceae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 12334)
Mite.O., Elsen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Wamanhewan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 12334)
White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D.,
Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L.,
Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 TGTCAGAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTCTTGTGTGGGCCTGCTCATTG 109
                                                                                                                                        Coordination of murine parotid secretory protein and salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 TGTCAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans R1 section 102 of 229 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GGAACTCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 GGACCTCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1%; Score 62.6; DB 10; 73.4%; Pred. No. 3.9e-06; Bilve 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Psp"
/note="first expressed exon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 286 (5444), 1571-1577 (1999)
                                                                                                                                                                                                                                                                                                       /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12334 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 g
+ 1.
                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="spleen"
                                                                                                                                                                                                                                                                                                                              /strain="C3H.Amy-YBR"
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                       amylase expression
EMBO J. 5, 1891-1896 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              About 720 bp after segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:6458892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Psp"
185. .>210
/gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE001965 AE000513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         radiodurans R1
```

```
/translation="MTRTPLTLEQLNALSDDAFTEHFAGVLEHSPHYARRAAAGRPFA
DVEEVAAAFARAVAADEPGAQVQLIRAHPDLAGKAALAGELTAESASEQTSAGLDRLS
PEEYAEFQRLNAAYHERFGLPYVVCVRENTKDTIFEGARRRLTHTQEEEQAAALHEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to PID:805293 percent identity: 62.08; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKKACLSASTTYRLLETLRQQGYVEWEERSGLFSVGLRAYQVGAAFSERNSLLSAAGA
VMQALVEEVNETANLAVLRGNEAVYVHQVEASQLMRMFTHIGAAAPLHCSGVGKVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLERLHAALGREIERTYAASGLNAAGWDLLLTLYRSAPPEGLRPTELSALAAISGPS
TSNRIVRLLEKGLIERREDERDRRSASIRLTPQGRALVTHLLPAHLATTQRVLAPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mwtgtqqpgtqpkvkvklgbnvygkabvqlmkikkgtpRhElrB
AKVRVAMYGDFGAAHSEGDNTDLVATDTVRNTVYGLAKEGFESSIEEFGKELLTHFVK
                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTEAPKLKSGRARSGEAGSVRTLERGLSVLSALAELREATLTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLPPAEVRRKVGDGPFPAYTPHSITTLAALTRELNTVRGQDYALDDEERELGVRCLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSARMDNDTAALLERIRSDWARLNHGQGPDSDGLTPSAGPMLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGPRVTGGFAEFTEHLWERVQTPAQPQGHDHAFVRQMPKRTARVETQDGRRFTVTSGI
EELYVLKTTESGWENYLLDERFTTLPETHDRVMATFVTAKWEYAVESCDYDAVWERYY
RQIQHTFTDHYSPSLQRTLXLMGEAVLSVCPEISRIWFQMPNKHHLVYNLGRFGLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity: putative:hydroxypyruvate reductase, putative,
authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:X74409 SP:P42195 PID:396458 percent identity; 56.72; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P34798 PID:432629 percent identity: 57.45; identified by sequence similarity; putative"
                                                                                                                                         /note="similar to SP:P37728 GB:X62072 PID:48982 percent identity: 58.17; identified by sequence similarity: putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AL009126 percent identity: 58.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVRAASGEVVASLSVSAPISRFPKKNIPDMLGRVQAASEQISARLGWRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="transcriptional regulator, MarR family"
/protein_id="AAF10732.1"
/db_xref="GI:6458898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="AAF10731.1"
/db_xref="G1:6458897"
                                                                                                                                                                                                                                                                                                                                /product="transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIARLRILDLVQEGRQEKRMDGRLIRIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAF10733.1"
/db_xref="G1:6458899"
                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF10730.1"
/db_xref="GI:6458896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5161. .6392)
/gene="DR1157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7360. .7905)
/gene="DR1159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEILHVDPEPYGLMEAWVERAE"
                           complement(4153. .4956)
/gene="DR1156"
                                                                                         complement(4153. .4956)
/gene="DR1156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7360. .7905)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEORTLEELAGRMLAGLEOGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"uricase"
                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="DR1158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="DR1158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DR1159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DR1160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8007. .8903
/gene="DR1160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                  /codon_start=1
   QRLHLSSDSEKPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      authentic
6657. .722
                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dene
                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNETQAAQLTRQVIDTCDALACHTEVPGEITRTYLCPTTRQVHE
ELAANADRLGMTTRVDAVQNILBSRLESRAPGAFTLY IGSHLDTVPNARDVEIGTVVF
GYALVEARENETRERLEPHLEVLGFSEEFEVPRYGVSFIGSRALVGTADELLTVSDRENQTV
RDAIVGYGLNPDELPGAGAEDRPLCYLEIHTRQGPVLQDQGAANGVVSAIVGQSRLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MSLDLLLRGAVLVTPEGERRADLGIVGGQIAELTDEIATPAAQT
LDVSGLHVFPGVLDDHVHLNEPGRTHWEGFETGTQALAAGGATSFLDMPLNSSPPVLT
RERFEDKARLGEEKSLIDFGLWGGLTPLNLDQLDDLAECGVIGLKAFMSHSGLDEFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAVORALLERQDTGAALHLVHYSSGAAVALAYEGKÖKGIDVTTETCEHYLHFTGEDVE
RVGAALKCAPPLRDPAVQEELWRELLAGHIDTVGSDHSPAPPDMKTSEDFFSLWGGIS
GAGSTLNVMLEDGYAQRGLPLE1IAALLALNPAQRFGLPQKGRLAVGADADFALVALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P37113 GB:S67784 GB:X74289 PID:460895 SP:053389 percent identity: 55.20; identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGEVSCSLDIRHADDAVRAGSLOELLALAEREAAARQVACSVTPRMAEAAVPMAPSLR
ALLHQAAERGGUTHPELVSSGAHDAQIMAQKWPAAMLFLRSPNALSHHPDEMAEPGDV
AAGIRVGTRFLELLAAQAEQQVQA"
complement (2698. . 4089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mnPPPLSLSPAALALAROLHTRLRDRWAGLPGEPPARANSVLTA
ARAAATPDDEGRRABELIVERSDLDMHERAVDSDAAVVDEPDDFFSFTRDWYQASD
ALAWVAESDRPLLARTRALVALEPHLDFDGPAIAALCDLSAVLAARPERPIHTYVPKL
ETPARAQFWHDALLLAEEHLSLAPNTVKTCLQIETFSGLLNIEAVFEPLAPRTYGLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDLTLYEGMRTAKRHGLVVATHAESNEFTRRLTETARAQGKSGVRDYLESRPVVTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P08997 GB:X12431 PID:396349 PID:40887 GB:U00096 percent identity: 49.74; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRWDYVËSLTKHLGTRRDTPMPPRSQLTMDVDAMRAYAETLVRVCRAHGAEAIGGTAS
FAPDPQNSQPALGAVLADKQREAAQGFTAAWAGLPELLEPVRRGFDAPAGSENKDTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLYHRLTDLPDPGPLRLADVREALEIALGVFAAWYRGEGVLVRAGRIEDTATAELARA
OLWGWVRVRAALEDGERLTPERYRQERRAVLGDDEPASRLLDHLVEAPACAAYFPLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFTGRASHAGTTPMHLKRDALAAAARFIVGAEDLANKTPGLVATVGMIEAKPGAGNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKFTLDTLYDRWQQNPYRGQSFQGRVHATYLRGQPVYQNGEFTGTPRGRLLRPRSL" complement(1451. .2701)
                                                                                                                            Direct Submission
Submitted (08-NOV-1999) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Minton,K.W., Fleischmann,R.D., Ketchum,K.A., Nelson,R.E., Salzberg,S., Smith,H.Q., Venter,J.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notes"similar to GB:U00096 SP:P77671 PID:1773192 PID:177822 percent identity: 64.13; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="N-carbamyl-L-amino acid amidohydrolase"/protein_id="AAF10728.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="malate synthase, putative"
/protein_id="AAF10729.1"
/db_xref="G1:6458895"
                                                                                                                                                                                                                                                                                             /organism="Deinococcus radiodurans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="allantoinase, putative"
/protein_id="AAF10727.1"
/db_xref="G1:6458893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1451. .2701)
/gene="DR1154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2698. .4089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(108. .1454)
/gene="DR1153"
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(108. .1454)
                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:6458894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene-"DR1153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DR1154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="DR1155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="DR1155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start*1
                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="1
                                                                                                                                                                                                                                                                                                                                /strain~"R1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity;
                                                                                                                                                                                                                                                                  .12334
                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCC
```

```
29056 a
                                                                                                                                   11694876
                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                       JOURNAL
                                                                                                                                   PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                           FEATURES
                                           TITLE
                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                             /translation="MSGHPGLTTHVLDTARGKPAAGVRVQLCRVTGDTRTPVTEAVTN
SDGRTDAPLIERGSLKGGTYELTFHVADYFKGFVAAADPPFLDVVTLRFTVGDTSGHY
HVPLVMTPWSYSTYRGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mtrepvrmtrockerlebolovlkttrreoisevmgkalebobl
resaaydearmooseneakiaeleaqleraqimkdeeldtsavgvgarvivedaqnko
rtleivgsfevdylkgkisdaspmgqallgkrpgesavwpgpkgnvslkvisveyp"
                                                                                                                                                                                                                                                                                                                                                                                                                            PID:606119 percent identity: 62.03; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to SP:P21346 GB:U01376 GB:X54718 PID:41611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 125020) Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10511 CCTATCACATTCTGACCATCGAAGACCCCATCGAGGTGCTGCACCGCAACAACGCGCAGTC 10452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10391 CGCTGCGTCAAGACCCCGACGTGATCGTGATCGCGGGGATTCGGGAACGGGAAACGGTGG 10332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10331 AGGCCGCGTGCTGGGGGGGCGAGACCGGGCATCTGGTCATCAGCACCCTGCACACCCAGG 10272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10571 CCGGCAGTGGCAAGACCACCACGTCGCCAGCCTCATCGACTACCTCAACCGGCACTTCG 10512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AL009126 percent identity: 63.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 TTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611 AACACCACAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 PATCCTCCTCCTCCAGAAGGAGATATGTCCACTGATCGCCATCTTCATCCACTCCCTGG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 CTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 CCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCAGCCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 12334;
                                                                                                          identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF429315 125020 bp. DNA linear P
Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="transcription elongation factor"
/protein_id="AAF10735.1"
                                                                                                                                                                     /product="conserved hypothetical protein" /protein_id="AAF10734.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 46.2%; Pred. No. 1.6;
Matches 141; Conservative 0; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 42.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9895, .10968)
                                                                                                                                                                                                                                                                                                               complement(9370. .9846)
/yene="DR1162"
                                                                                                                                                                                                                                                                                                                                                    complement(9370, .9846)
/gene="DR1162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity; putative"
                                                                                                                                                                                                                          /db_xref-"GI:6458900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:6458901"
                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
         /gene="DR1161"
8900. .9259
                                                          /gene="DR1161"
                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF429315.1 GI:17646244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 10271 ACGCG 10267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       731 ATGTG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                      dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dene
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                         CDS
                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
1 32731 c 30696 g 28283 t 4254 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                             Holmes, S.E., Ingersoil-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17312 KCCWCMKMCYCMMRSMRSRGMSYYMYASWKSSSRGCYCTRCYWCMSSKSCYKSYYMMMRS 17371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17372 KRMKGMKWSRCWGSMWGSASRSSCYK-CYKSMRCSMMSSKCYRCAGCMMMKGGYMRYMRC 17430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17491 MKCASYMCMSSYWCTCWCTSYMSYYRCTCWCKGWSSYTKSKSWSSSMSSYKKGRRKSYSM 17550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17431 WSMKRRWWGKSAMYRMRRMWKGRGAMMMCMKCYSRWSRCMMMMKSYCASCRSCAMMSGTY 17490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17551 CCTSRGAMSCWRRCCYMRGASSMRAGSMSRRRAKGRSWGGRSKWWMTGGMWRSKYYYYCT 17610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 17252 SCRAGMSCTKYKSSMTMSMASYCWCMSMYYCSMRSMASRGMSWSSYMKMMKSSWRMSCYM 17311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 ACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACAC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 ACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 TGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 AAAGCACTGTTCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 TGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 ACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         Stevanin, G., Brice, A.,
Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margolis, R.L. A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 NAt. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="isolated from a patient with Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 41; DB 9; Length 125020; 11.4%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="16q24.3; between D16S520 and WI-12410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="junctophilin 3" complement(<36507, ,>36887) /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 239; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(35581, .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                  (bases 1 to 125020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_unit=ctq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disease-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="JP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
```

q

δ pp

õ

```
gene
                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                RESULT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                             LOCUS
                                                                                    q
                                                                                                                 ò
                                                                                                                                           g
                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='human lung Marathon-Ready (TM) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG1K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
C12N15/00,
                                                                                                                                                                                                                                            PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
CIZNIS/09,CO7K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 TCARAGCTGARGGATGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACGCGA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 PTGGCCTTGTGCAGGCCTGATGGCCACGGTCTCTATGTCACCATCCCTCTGGGCATAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 ATGTCACTGTGGGCGCGGTCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IGCTICCAACTAACAGGACAȚITITGGGTIGAAAATCAGCAACTCCCTCATCCTGGATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 TGATICCIGGCCIGAACAACATCATIGACATAAAGGTCACTGACCCCCAGCTGCTGGAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17731 GKSKCWKRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCYSSMSCTSMYRCC 17790
                                                               17671 MKGMRGSCWSSKMWGGSHSRSBSSKCKGSRGMRRSKKSSKYRKRGRGKKRSMTKSKGSK 17730
17611 GREMMMTYMCCCWRRRSYMYYRSMSAMGMRKSSWSGMRNMGSASSRRCKSASRSSWCSRR 17670
                                                                                           842 TECCAGTGGCTTGCCCCACCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACC 901
                                                                                                                                                                                                                                                                                                                                                              Kadota.M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
LUNX gene and method for detecting micrometastasis of cancer
Patent: JP 2001078772-A 1 27-MAR-2001;
OTSUKA PHARMACEUT CO LTD
                                      782 TGCAAACCCTCATTTGAAGAAGGACGAATGAGGAGGACCACTGTGGTGCTGATTGGT 841
                                                                                                                                                                                                                                     768 bp DNA linear PAT 31-JF
LUNX gene and method for detecting micrometastasis of cancer.
E53840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.9%; Score 40.4; DB 6; Length 768; 45.8%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 human lung Marathon-Ready (TM) cDNA library
JP 2001078772-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/db_xref="taxon:32644"
217 c 204 g 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1999 JP 1999253186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                       Db 17791 WGGMKSYSTCGTTCKKCTGYKKS 17813
                                                                                                                                                             902 TAACCAGCGTGAAAGCCTGAGTC 924
                                                                                                                                                                                                                                                                                                   GI:18633610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A61K35/12, A61K35/76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 45.8
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                       E53840.1 GI:18633
JP 2001078772-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-200
                                                                                                                                                                                                                                                                                                                                 unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                         unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ರ
                                                                                                                                                                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                              VERSTON
                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                        E53840
                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
```

```
/Lranslation="MEQTGGLIVFYGLLAQTWAQFGGLPVPLDQTLPLNVNPALPLSP
/Lranslation="MEQTGGLIGILENLPLDILKPGGGTSGGLIGGLLGKYTSVIPGL
TGLAGSLINALSNGLLSGGLIGILENLPLLDILKPGGGTSGGLIGGLLGKYTSVIPGL
NNIIDIKYPPQLLELGLVQSFDGHRLYYTIPLGIKLQVNTPLVGASLLRAVKLDIT
NNIIDIKYPPQLELGLVQSFDGHRLYYTIPLGIKLQVTPLQGLLDSLTGILNKVLPEL
NKGNVCPLVNEVLRGLDITLVNDIVMLHGLQFVIKV"
285 c 258 9 243 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (28-JUL-1999) Molecular and Genetic Medicine, University
of Sheffield School of Medicine, Glossop Road, Sheffield S10 2RX,
UK
                                                                                                                                                                                                                                                                                                                                      PRI 02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 AIGTCACTGTGGCCGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 TIGGCCTIGIGCAGAGCCCIGAIGGCCACCGICICIAIGICACCAICCGICICGGCAIAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 TCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria;

Mammalia; Lo 1011)

1 (bases 1 to 1011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 TGCTTCCAACTAACAGGACATTTTTGGGTTGAAAATCAGCAAGTCCCTCATCCTGGATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 TGATTCCTGGCCTGAACAACATCATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAAC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bingle, C.D. and Bingle, L. Characterisation of the human plunc gene, a gene product with a characterisation of the human plunc gene, a gene product with a upper airways and nasopharyngeal restricted expression pattern Biochim. Biophys. Acta 1493 (3), 363-367 (2000)
                                                                                                             533 GTGACTGCACCATTCCCCTGGAAGCTGCTGATTCTCTGCTTGATGGACTTGGCCCC 592
                                                                                     563 GAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAA 622
                                        473 ACATCACTGCAGAAATCTTAGCTGTGAGAGATAAGCAGGAGGAGGATCCACCTGGTCCTTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="enriched in tracheal and nasal epithelium"
503 TCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACCAGCCTGTTGCCGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 40.4; DB 9; Length 1011; 45.8%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                            Homo Sapiens PLUNC (PLUNC) mRNA, complete cds. AF172993
                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF70860.1"
/db_xref="GI:7958616"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="PLUNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PLUNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                 AF172993.1 GI:7958615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 45.89
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 a
                                                                                                                                                                                                                 623 TCATCA 628
                                                                                                                                                                                                                                                            593 TCCCCA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , пашап
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
```

The state of the s

ö

多罗:

多爱

. . . **M**. .

- - 503 TCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACGAGCCTGTTGCCGTCCTGG 562
- ŏ
- ŏ
- - 623 TCATCA 628 ζ.

۲۷

iearch completed: August 6, 2002, 17:26:32
fob time: 5124 sec

BGB70257 602791125 BGB70258 602792873 BGB71619 602792811 BGB71159 602792447 BGB67154 602786768 BGB72659 60279317 BGB67869 60279317

BG870257 BG872058 BG871297 BG871297 BG872659 BG872659 BG872659 BG872659 BG872659

602791676

AA792682 vs75b09.r BC869519 602789531 BC869465 602789159 BC867228 602789189 BC86588 602789649 BC871442 602793489 BC865861 6027896280 BC865861 602788280 BC865861 6027881804 BC866924 602786167 BC866944 602786167 BC866944 602789145 BC869454 602789145 BC869454 602789145

BG869519 BG869465 BG867259 BG870228 BG869588 BG871442 BF535510

BG865641 BG866924 BG869454 BG87130 BG871864

100 100 100 100 100 100 100

BG872117 6 BG870254 6 BG871444 6 BG870889 6 BG866908 6

ALIGNMENTS

```
August 6, 2002, 14:03:33; Search time 1685.42 Seconds (without alignments) 8232.292 Million cell updates/sec
                                                                                1028
1 CACGAGATTICATGAGCATC.....AAGGCCCATTTCTGCAAAA 1028
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                         13736207 seqs, 6748477542 residues
                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                 nucleic search, using sw model
                                                                                                           Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                  em_gss_inv:*
em_gss_pln:*
em_gss_vrt:*
                                                                                                                                                                                                                                                                             gb_htc:*
gb_gss:*
em_gss_hum:*
                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                        US-10-020-139-1
                                                                                                                                                                                                                 em_esthum:*
em_estin:*
em_estin:*
em_estp1:*
em_estro:*
em_hestin:*
gb_est1:*
                                                                                                                                                                                                           en_estba:*
                                                                                                    IDENTITY_NUC
                                                                                                                                                                                                     EST: *
                                                                                                                                                                                                           Perfect score:
                                                                                                     Scoring table:
                                 OM nucleic
                                                                                        Sednence:
                                                                                                                                                                                                     Database
                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

BG86528 6027894.2 BG87214 60279120 BG87214 60279120 BG87214 602792983 AK009032 Mus muscu BG87446 BC8792782 BG8654 Mus muscu BG865328 602782782 BG865328 60278333 BG86534 60278123 BG865768 60278123 BG865768 60278138 BG865768 60278438 BG865768 60278438 BG865768 60278438 BG865768 60278438 AI654622 wb48fll.x AI218468 qh27e04.x Description A1218468 BGB69528 BGB70334 BGB72145 AK009032 AK010181 BG872461 AK009654 BG865328 BG865874 BG870337 BG865768 BG865768 BG868020 BG869767 BI688385 Query Match Length DB 388 891 8891 8891 8972 972 972 972 973 973 973 973 973 973 973 973 Score 341.4 2218 200.8 1990.8 198.4 198.4 195.8 1195.8 1195.8 1195.1 197 8 0 0

	RESULT 1 A1654622 LOGUS DEFINITION wb48f11.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2308941 3', ACCESSION A1654622 VERSION A1654622 I GI:4738601 KEYMORDS EST. SOURCE Duman	ORGANISM Homo sapiens Eukaryota: Mammalia; Eutheria; Eutheria; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 384) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TUMOR Gene Index.		FEATURES Location/Qualifiers 1. 384 / Organism="Homo sapiens" / Ab_xref="taxon:9606" / Clone="InAGE:2308941" / Clone=Lib="NCI_CGAP_GC6" / tissue_Ltype="pooled germ cell tumors" / Tab_host="D9108" / note="Vector: pT7730-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
--	--	---	--	--

us-10-020-139-1.rst

ORIGIN

g

ò g ò

ò qq ô

```
from the normalized library NCI_CGAP_GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1228631, 1469064-1470983, and 147592-147673). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1845918"
/clone_lib="Scares_NFL_T_GBC_S1"
/lab_most="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 472 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        670 GTATCCTCCCTGCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCACTCCCTG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      790 CICATITGAAGAGGACGAAIGAGGAGGACCACIGIGGIGCAIGCIGAIIGGIICCCAGIG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   850 GCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 GCTTGCCCCCCCCCTTATAGCATTTCCCTCCAGGAAGCTGCTGCCCCCCCTAACCAGG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 ACAGCAGCCTGTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 GTATCCTCCCTGCTGCTGAGGAGGAGTATGTCCACTGATCCGCATCTTCATCCACTCCCTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730 GATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910 GTGAAAGCCTGAGTCCCACCAGGAAGGACCTTCCCAGATACCCCTTGTCCTCACAGTCAGA 969
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ACAGCACCTCTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTTGCAAAAA 26
                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI218468 253 bp mRNA linear EST qh27e64.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845918 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                             DB 9; Length 384;
                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                             Score 341.4; DB 9
Pred. No. 1.6e-80;
                                                                                                                                                                                                    112 t
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: -400P from Gibco
                                                                                                                                                                                                 119 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1218468.1 GI:3798283
                                                                                                                                                                                                                                                                                                                   33.2%;
96.9%;
                                                                                                                                                                                                    72 C
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI218468
                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                       Matches 348;
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI218468/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESS 10N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
```

KEYWORDS

Locus

du

ó g

qq ò SOURCE

TITLE

COMMENT

FEATURES

```
Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCL_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR=amplified conns from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-30207, 682632-687239, 1.M.A.G.E. 28711, and 729096-731399, Subtraction by Bento Soares and M. Felima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (Tl phage-resistant)"
/note="Corgan: salivary gland; Vector: pCMV-SPORT6; Site_l:
NotI: Site_2: Sali; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb, Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG869528 891 bp mRNA linear EST 29-MAY-2001 602789545F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4921042 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Thissue Procurement: Jeffrey E. Green, M.D.
This Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIOSS Frow: I column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              803 GACGAATGAGGAGGACCACTGTGTGTGTAGTTGGTTCCCAGTGGCTTGCCCCACCC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GACGAATGAGGAGGACCCCTGTGGTGCATGCTTGCTTCCCAGTGGCTTGCCCCACCC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            863 CCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 TCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 TCCCCCCAGAAGGACCTTCCCAGATACCCCTTTTCCTCACAGTCAGAACAGCAGCCTCTA 74
                                                                                                                                                                                                                                                                                                                                                                                                            Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                983 CACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%; Score 218; DB 9;
97.8%; Pred. No. 1.2e-47;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                     Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4921042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                          77 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG869528.1 GI:14220068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 891)
                                                                                                                                                                                                                                                                                                48 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG869528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG869528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

q ó g ò g ά QQ δ ΩD ò Db ò g ô q

```
/clone="IMAGE:4922525"
/clone_lib="NCI_CGAP_SG2"
/labulow_TI phage-resistant)"
/note="Organ: aalivary gland; Vector: pCMV-SPORT6; Site_l:
NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
602791220F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922525 5'
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------AAATTCTGAATCCTCCTCTGAAGCTGTCCCTCAGAAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGTTGGCCATTAGCCAAGAACAGC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 AATGGTTTATTGTTGAAAATCAATAATCTCAAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 362
                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTCTTGTGTGGGCCTGCTCATTGGGAAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TCAGAGTCACTTCTTGGTGAACTTGGCAGGGTGTGAATAATTTGA--------147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ATTCTAGAAACGTTGAACACAGCGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 GACATTTTTGGGTTGAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%; Score 199.8; DB 10; Length 896; 55.6%; Pred. No. 1.7e-42; Live 0; Mismatches 337; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10842 row: g column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 893.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
                                                                                             BG870334.1 GI:14220874
                                                                                                                                                                                                                                                                                           (bases 1 to 896)
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .896
                                      mRNA seguence.
                                                                                                                                                                                          Mus musculus
                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
DEFINITION
                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                 ACCESSION
                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGGTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGGTCCTGGATTTTCAAGCTGAGAGGTCT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTTGCTGCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGCC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       719 AATCTACTTGGCAGGA -- CAGGTACAACTTGCCCTCTGAAGAAGGAAGAAGGATG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 GACATTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 GATGGTGTCTCTACCCTCCTTACAAGTACATTGTCAACGTCCTCCAAAACTTGCTATGT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGGTCTCCTCTT 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 CCACAATCTCCTGCTGGTAACTCTCCAGTGGTTCAATCTTACTTCTGATGGCATTTCCTT 836
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                           40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                         38 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTTGTTGTGGCCTGCTCATTGGGAAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 ATTCTAGAAACGTTGAACACAGGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC
Technologies. Note: this is a NCI_CGAP Library.
                                                                                                                                                                                                                             41;
                                                                                                                                                           Length 891;
                                                                                                                                                                                                                      0; Mismatches 347; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                        DB 10;
                                                                                                                                                           Score 200.8; DB 10
Pred. No. 9.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 CCAGGAAGCTGCTGCCACCTAACCA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       837 CITAGAAGIGCIACIATCAICCACACA 864
                               175 9
                                                                                                                                                           19.5%;
55.3%;
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                              Local Similarity
                               232 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG870334
                                                                                                                                                                                                                                480;
                                                                                                                                                               Query Match
                           BASE COUNT
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG870334
LOCUS
```

g ò q ò g ò g ò

δ

RESULT

g

q ò

ä

```
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: salivary gland; Vector: pcMv-SPORT6; Site_l:
Not1; Site_2: Sali: Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG872145 844 bp mRNA linear EST 29-MAY-2007 602792983F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4924053 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgupbs-r@mail.nh.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics. Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
520 ATTGAAACTGATCCCCAGACACACCAGCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                  580 CCAACCAGCATCTCACTFFCCTTGCTGGACAACACAGCCAAATCATCAACAGTTCGTG 639
                                                                                                                                                                                                                              543 ACAGATAAAATCTCCATTTTCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 602
                                                                                                                                                                                                                                                                                  640 AATAGGGGGGGATCAACACGCGGGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAATATGT 699
                                                                                                                                                                                                                                                                                                                                    603 GATGGTCTCTACCTCCTTACAAGTACATTGTCAACGTCCTGCAAAACTTCCTATGT 662
                                                                                                                                                                                                                                                                                                                                                                                        700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                 760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                 183 ATTAAAACCAATCCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780 CCACAATCTCCTGCTGGCTACTCTCCAGTGGTTTCATCTTACTTGTGATGGCATTTCCCT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM10846 row: f column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 844)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4924053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG872145.1 GI:14222685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 880 CCAGGAAGCTGCT 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840 CTAAGAAAGTGCT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BG872145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
BG872145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESS 10N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                 Dp
Dp
                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                               ò
                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
```

```
<u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK009032 972 bp mRNA linear HTC 19-JAN-20 MUS musculus adult male tongue CDNA, RIKEN full-length enriched library, clone:2300005806:parotid secretory protein, full insert
                                                                                                                                                                                                                                                                                        160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                       220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ATTCTAGAAACGTTGAACACAGCGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 GACATTTTTGGGTTGAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 GATGATGGCCAAAGGCCTTAACCTGAGCTTCCCTGTCACGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 ATTGAAACTGATCCCCAGACACACCCCGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 ATTAAAACCAATGCCCAGACTGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTGGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGGTGTTCTTCAGGGTCTCCTCTT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTGATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 ACTGIGGIGCATGCTTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 TCAGAGTCTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                          92 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------- 137
                                                                                                                                                                                                                                                                                                                                    138 -----AAATTCTGAATCCTCCTCTGAAGCTGTCCTCAGAAC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                   176 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 235
                                              41; Gaps
                                                                                            40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                             32 AAACCAAAGAIGTICCAACTIGGGAGCCTIGIIGITGTGTGGGCCTGCTCATTGGGAAC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 AATCTACTGGGCAGGA--CAGGTACAACTTGCCCTCTGAAGAGAGAGAGAAGAAGATGC
                                                                                                                           DB 10; Length 844;
                                              0; Mismatches 336; Indels
  Score 198.4; DB 1
Pred. No. 3.9e-42;
19.3%;
                                              Matches 471; Conservative
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         880 CCAGGAAG 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       831 CTAGAAAG 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sednence
     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK009032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                          q
                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                        à
```

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Se Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carinforlo, P., Eukuda, S., Fukunishi, Y., Furuno, M., Hangarki, T., Hara, A., Hayatsu, M., Hill, D., Hiramoto, K., Hiracka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salio, R., Salio, R., Sana, I., Salio, R., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Silibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T., Tanaka, T., Tanaka, T., Tajami, R., Tayami, R., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                Carning, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., 1toh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishino,T., Harda,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yaliakak,S., Inoue,K., Toqawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, 330-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                  Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2300005B06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
S (bases 1 to 972)
                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia;
AK009032
AK009032.1 GI:12843579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                 HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           further details.
                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (sites)
                                                                                                                                                                                                                                               (sites)
                                                                                                                                                                                                                                                                                                                                                                                                              (sites)
                                                                                                                                                                                                                                                                                                                                                                              10349636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11042159
                                                                                                                                                                                                                                                                                                                                                       99279253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11076861
                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                SOURCE
```

```
and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGGATTATTAAATAGCCCCCCCCCCC 3']. CDNA was cleaved with XhoI and StI. Cloning sites, 5' end: XhoI; 3' end: StI.
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB26037.1"
/db_xref="GI:12843580"
/translation="MFQLGSLVVLCGLLIGNSESLLGELGSAVNNLKILNPPSEAVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NINLDVELLQQATSWPLAKNSILETLNTADLONLKSFTSLNGLLLKINNLKVLDFQAK
LSSNGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGK
CSSNTDKISISLLGRRLPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGAGTCTCTTGTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 ------AAATTCTGAATCCTCCTCTGAAGCTGTCTGAACCTCAGAAC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ATTCTAGAAACGTTGAACACAGCGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 GACATTITIGGGTIGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 GATGATGCCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACGGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="data source:MGD, source key:MGI:97787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 198; DB 11; Length 972; 55.7%; Pred. No. 5.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 t
                                                                                                                                                                                                                                                                           /db_xref="MGD:MGI:1898546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parotid secretory protein
                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="2300005B06"
                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tongue"
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOGILSNILAGOVOLAL"
                                                                                                                                                                                                                                                    /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evidence: ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dene="Psp"
                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                          Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dene
                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

us-10-020-139-1.rst

```
(sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
  PUBMED
                            REFERENCE
                                                       AUTHORS
                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibate, K. Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonake, S., Inoue, K., Togawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carningi,P., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Pormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNAs libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus adult male tongue CDNA, RIKEN Eull-length enriched library, clone:2310075K06:parotid secretory protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             880 CCAGGAAGCTGCTGCCACCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (strain:C37BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2310075K06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               786 CACAACTCTCCTGCTGCCTACTCTCCAGTGCTTTCATCTTACTTCTGATGCATTTCCCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 CTAGAAAG----TGCTACTATCATCCACATTTCTACCTGAG-ACCACCCAAAGGACCC 900
609 GATGGTGTCTCTACCTTACAAGTACATGTACAACGTCCTGCAAAACTTCCTATGT 668
                                                                                                                                                                                                                                                                                                                                                                                                          760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 AATCTACTG---GCAGGACAGGTACAACTTGCCCTCTGAAGAGGAAGAACAGAAGGATGC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCTTATAGCATCTCCCT 879
                                                                                 580 CCAACCAGCATCTCACTTTCCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                 700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                669 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGGTCTCCTCT 728
                                                                                                                                                                                      640 AATAGCCTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, p. and Hayashizaki, y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      972 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK010181.1 GI:12845441
HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 TCCCAGATACCCCTTCTC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 receAATTETETTETE 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK010181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10349636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK010181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99279253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11042159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORCANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURHAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDL I NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK010181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERS TON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
```

q

qq ò g

ò

g

qq ô a ô

```
S. Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Pukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, M., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Sand, M., Coya, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tanaka, T., Tapami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tajima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yashidaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rranilation-"MFQLGSLVVLGGLLIGNSESLLGELGSAVNNLKILNPPSEAVPQ
NNLDVRELLQQATSWPLAKNSILETLNTADLGANLSFTSLTGLLLKINNLKVLDFQAK
LSSNGWGIDLTVPLAGGASLVLPFIGKTWDISYSLDLINSLSIKTNAQTGLPFYTIGK
CSSNTDKISISLLGGRRLPIINSILDGVSTLLTSTLSTVLQNFLCFLLQYVLSTLNPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           physical and Chemical Research (RIKEN), Laboratory for Genome physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, RELISTE,//Genome-gsc.riken.go.jp, Tel:81-45-503-9216, Pax:81-45-503-9216, Pax:81-45-503-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome correction because the Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGAAGATCTATTTTTTTTTTTTVN 3'], cDNA was
The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="data source:MGD, source key:MGI:97787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="MGD:MG1:1898576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parotid secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB26753.1"
/db_xref="G1:12845442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /orqanism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:10090"
/clone="2310075K06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOGILSNILAGOVQLAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evidence: ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 c
                                                                     FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene=
57...7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sedneuce (5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Host: SOLR.
```

BG872461

Gaps

```
580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACACAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCACCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 ACTGIGGIGCAIGCIGATIGGITCCCAGIGGCTIGCCCCACCCCCTTAIAGCAICTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 CACAACTCTCCTGCTGGCTACTCTCCAGTGGTTTCATCTTACTTCTGATGGCATTTCCCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 CCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      846 CTAGAAAG----TGCTACTATCATCCACATTTCTACCTGAG-ACCACCCAAAGGACCC 900
                                                                                                                                                                                          48 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTCTTGTGGGCCTGCTCATTGGGAAC 107
                                                                                                                                                                                                                                        100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                  160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                 ------AAATTCTGAATCCTCCTCTGAAGCTGTCCCTCAGAAC 191
                                                                                                                                                                                                                                                                                                                                                                                                              220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 CTGAATCTGGATGTGGAGTTGGTTCAGCAAGCTGGCCAAGTTGGCCATAGCCAAGAACAGC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ATTCTAGAAACGTFGAACACAGGGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 ACAGATAAAATCTCCATTTCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                  40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGAACC 99
                                                                                                        Indels 47;
                                                              Length 972;
                                                                                                        0; Mismatches 360;
                                                            Score 198; DB 11;
Pred. No. 5.4e-42;
                                                            19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 TCCCAAATTCTCTTCTC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 TCCCAGATACCCCTTCTC 957
                                                                                                        Conservative
                                                                                   Similarity
                                                                                                        511:
                                                                 Query Match
                                                                                                        Matches
ORIGIN
                                                                                                                                                                                            qq
                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                пр
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

RESULT

```
/clone_lib="NCI_CGAP_SG2"

/lab_host="DH10B (Tl phage=resistant)"
/hote="Organ: salivary gland; Vector: pCMV-SPORT6; Site_l:
Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
EST 29-MAY-2001
                  602792782F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923980 5',
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 CCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 -----AAATTCTGAATCCTCCTCTGAAGCTGTCAGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 ATTCTAGAAACGTIGAACACAGCGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 TCCAACGGCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGGGGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 AAACCAAAGAIGITCCAACIIIGGGAGCCIITGIAGICIIGIGGGCCIGCICAIIGGGAAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LNL at:
http://mage.lnl.gov.
http://mage.lnl.gov.
High quality sequence stop: 823.
                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 196.8; DB 10; Length 954; Pred. No. 1.1e-41;
linear
                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 372;
BRNA

    954
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4923980"
                                                                                            BG872461.1 GI:14223001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.1%;
54.8%;
                                                                                                                                                                                                                                                  (bases 1 to 954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                               mRNA sequence.
                                                                                                                                                                        Mus musculus
                                                                                                                                                 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
BG872461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                       DEFINITION
                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                       ACCESSION
                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                      KEYWORDS
                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evidence: ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Psp"
57 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex≖"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dene="Psp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative"
                                                                                                                                                                                         FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sednence [5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                 REFERENCE
                                                                  JOURNAL
                                                                                               MEDLINE
                                                                                                                   PUBMED
                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishli,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus adult male tongue CDNA, RIKEN full-length enriched library, clone:2310037B02:parotid secretory protein, full insert
                         880 CCAGGAAGCTGCTGCCACCACCTAACCAGGGTGAAAGCCTGAGTCCCACCAGCAGGAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (strain:C57BL/6J) adult male tonque cDNA to mRNA, clone_lib:RiKEN full-length enriched mouse cDNA library
460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                          520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                        474 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 533
                                                                                                                                                                                         580 CCAACCAGCATCTCACTTTCCTTGCTGGACAACACAGCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                       534 ACAGATAAAATCTCCATTTCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 593
                                                                                                                                                                                                                                                                                        640 AATACCGTGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                      594 GATGGTGTCTCTACCCTCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTGCTATGT 653
                                                                                                                                                                                                                                                                                                                                                                                    700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 AATCTACTG - GCAGGACAGGGTACAAATTGCCCTCTGAACGAGGAAGAACCGAAGGATG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 CACAATCTCCTGTTGGGTACTCTCCAGGGGGTATCATCTTACTTCTGATGGCATTTCCT 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCTTATAGCATCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, p. and Hayashizaki, y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      971 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK009654.1 GI:12844580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940 TCCCAGATACCCCTTCTC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        890 TCCGAAATATCCTTCCTC 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone:2310037B02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK009654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK009654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11042159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10349636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK009654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STOC.
                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
Acachi, J. Aizawa, K. Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C. Carninoi, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kohima, Y., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, R., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Saki, C., Sakai, C., Saki, C., Sakai, R., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tejina, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5] GAGAGAGAGATCCAAGACCTTTTTTTTTTTTTTVN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RirBi hitegrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA was cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Benomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer
                                                                                                                                                                                                                                                                                                                                                                     The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="data source:MGD, source key:MGI:97787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="MGD:MGI:1895176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parotid secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB26418.1"
/db_xref="G1:12844581"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="2310037B02"
```

```
/translation="MFQPGSLVVLCGLLIGNSESLLGELGSAVNNLKILNPPSEAVPO
NLNLDVELLQQATSWPLAKNSILETLNTADLGNLKSFTSLNGLLLKI NNLKVLDFQAK
LSSNGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAOTGLPEVTIGK
CSSNTDKISISILGRRIPIINSILDGVSTLLTSTLSTVLQNFLCPLLQYVLSTLNPSV
DQGLLSNLAGQVQLAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AAATTCTGAATCCTCCCTCTGAAGCTGTCCCTCAGAAC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 ATTCTAGAAACGTTGAACACGGGGCCTTGGCAATTTAAAAAGCTTTACATCT----TTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 GACATITITIGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGGGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 TCCAACGCAATGGCATTGATCTGACGGTGCCTTGGCTGGGAAGCCTCTTTGGTTCTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 CCAACCAGCATCTCATTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 GAIGGIGICICTACCCTCCTIACAAGIACAIIGICAACCGICCIGCAAAACTICCIAIGI 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             729 AATCTACTG---GCAGGACAGGTACAACTTGCCCTCTGAAGAGGAAGAACAGAAGGATGC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 CACAACTCTCCTGCTGGCTACTCTCCAGTGGTTTCATCTTACTTCTGATGGCATTTCCCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 CCACTGATCCGCATCTTCATCCACTCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669 CCATTGCTTCAGTACGTCCTCAGCACACTGATCCAAGTGTTCTTCAGGGTCTCCTCT 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                          47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC
                                                                                                                                                                                                                                                                                                                              19.1%; Score 196.4; DB 11; Length 971; 55.6%; Pred. No. 1.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 361;
                                                                                                                                                                                                                                         184 g
                                                                                                                                                                  /note="putative"
971
                                                                                                                                                                                                                  /note~"putative"
                                                                                                                                                                                                                                         260 c
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                    Matches 510;
                                                                                                                                                                                              polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 ----
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
/note="Organ: salivary gland; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                       BG865328 892 bp mRNA linear EST 29-MAY-2001 602783932F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910430 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia: Eutheria: Nodentia: Sciurognathi; Muridae; Euteleostomi; losses 1 to 892)

1 (bases 1 to 892)

1 (hases 1 to 892)

Nuth-MCO http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.column: 07
                           880 CCAGGAAGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 TCAGAGTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AAATTCTGAATCCTCCTCTGAAGCTGTCCCTCAGAAC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCAAGTTGGCCATTAGCCAAGAACAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AAACCAAAGAIGITCCAACTIGGGAGCCTIGITGICIIGIGGGCCIGCTCAIIGGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 347; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:4910430"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH108 (T1 phage_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 195.8;
55.1%; Pred. No. 2e-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism~"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 8 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                           BG865328.1 GI:14215868
                                                                                                                               901 TCCCAAATTCTCTTCCTC 918
                                                                                                      940 TCCCAGATACCCCTTCTC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           892
                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 474; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                              BG865328
                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                   ά
                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

```
BG865874 870 bp mRNA linear EST 29-MAY-2001 602788106F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4914193 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
1 (abases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                               293 AATGGTTATTGTTGAAAAATCAAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 352
                                                                                                                                                                                                                                                                                                                          533 ACAGATAAAATCTCCATTTCCTTGTTGGGAAGACGATTACCCATCATCAACAGTATTCTG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 AATAGCCTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 GATGGTGTCTCTACCCTCCTTACAAGTACATGTGAACCGTCCTGCAAAAACTTCCTATGT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGGTCTCCTCTT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 AATCTAACTGGCACGGACAGGTACAACTTTGCCCTCTGAAGAGGAAGAACAAGGATGC 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         820 ACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGC - CCCACCCCCTTATAGCATCTCCC 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 CACAAATCTCCTGCTGGCTACTCTCCGGTGGCTTTCATCTTACTTCTGATGGCATTTCCC 832
236 ATTCTAGAAACGTTGAACACGGGACCTTGGCAATTTAAAAAGGTTTACATCT---TTG 292
                                                                                340 GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGGTG 399
                                                                                                                                                                                                                                          CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                       520 ATTGAAACTGGTCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACACCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                    400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLAM10820 row: 1 column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 858.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                879 TCCAGGAAGCTGCTGCCACCA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833 TCTAGAAGGTGCTATTATCA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG865874.1 GI:14216414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG865874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                            셤
                                                                                                                                g
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                ò
                                                                                                                                                                                      ^{\circ}
                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Source

```
286 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTTCAAGCTAAGCTGTCT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 CCCATCATIGGCCAGATTATCAACCIGAAAGCCTCCTIGGACCICCTGACGGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 ACAGATAAAATCTCCATTTCCTTGTGGAAGACGATTACCCATCATCAACAGTATTCTG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 -------AAATTCTGAATCCTCCCTCTGAAGCTGCCTCAGAAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 ATTCTAGAAACGTIGAACACAGCGGACCTIGGCAATTIAAAAAAGCTITACATCT---TIG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 GACATTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 TCCAACGCCAATGGCATTGATCTGACGCTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 ATTAAAACCAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACACCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 GATGGTGTCTCTACCCTTACAAGTACATTGTCAACCGTCCTGCAAAACTTCCTATGT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 CCATTGCTTCAGTACGTCCTCAGCACAGTGATCCAAGTGTTCTTCAGGGTCTCCTCTCT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706 AATCIACIGGCAGGACAGGIACAACTIGCCCTCIGAAGAGGAAGA--ACAGAAGGAIGCC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 ACTGTGGTGCATGCTGGTTCCCAGTGGCTTGCCCCACCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 AGACAAAAGAIGCTICAGCTITGGAAACITGITCTCCTGIGGGGGGGGGTGCTCACIGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTTGTTGTGGCCTGCTCATTGGGAAC 84
                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                      Length 870;
                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 195.2; DB 10; Length 55.3%; Pred. No. 2.9e-41; ive 0; Mismatches 338; Indels
/organism-"Mus musculus"
                                             /db_xref="taxon:10090"
                     /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 55.3%;
Matches 469; Conservative
                                                                                                                                                                                                                                                     223 a
                                                                                                                                                                                                                                                     COUNT
                                                                                                                                                                                                                                                  BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
BG872403 910 bp mRNA linear EST 29-MAY-2001
602792704F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4924056 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bace; to 910)
NIH-MG http://mgc.nci.nih.gov/.
340 GACATTITIGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM10846 row: g column: 01
                                                   294 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 353
                                                                                                   400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                     460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                      520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGGAGAATGCGGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                       580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                  700 CCACTGATCCGCATCTTCATCCACCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                  414 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 473
                                                                                                                                                                                                                                                                                                                                                      474 ATTAAAACCAAATGCCCAGACTGGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGGTCTCCTCTT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             760 AATCCTCAGCACAAAACCCAGGTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 ACTGTGGTGCATGCTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  774 CAAAAATCTCCTGCTGCTACTCTCCAGTGGCTTCATCTTACTTCTGATGGCATTTCCCT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 CCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   834 CTAGAAAG----TGCTACTATCATCCAGAATTTCTAACTTGGAAACCACGCAAAGGACCT 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    940 TCCCAGATACCCCTTCTCCTCACAGTCAGAAC 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       890 CCCAATTCTCTTCTCTGAGTAGTTCCAAC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 756.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG872403
BG872403.1 GI:14222943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG872403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG872403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                             g
                                                                                                 ò
                                                                                                                                                 q
                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_SG2"
/lab_host="DA10B (T1 phage resistant)"
/lab_host="DA10B (T1 phage resistant)"
/note="Vorgan: allivary gland; Vector: pCMV-SPORT6; Site_l:
NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
1 248 C 248 C 276 L
                                                                                                                                                                                               BG870337 968 bp mRNA linear EST 29-MAY-2001 602791223Fl NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922669 5',
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 ATTCTAGAAACGTIGAACACAGGGACCTIGGCAAITTAAAAAGCTTTACAICT---ITG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 193.6; DB 10; Length 968;
53.6%; Pred. No. 8.1e-41;
Live 0; Mismatches 389; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGGGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTCTTGTGTGCCTGCTCATTGGGAAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: LLAM10842 row: m column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:4922669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
                                                                                                                                                                                                                                                                                              BG870337.1 GI:14220877
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 53.69
Matches 500; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .968
                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                    ponse monse
                  880 CCAGGAAG 887
                                                                   824 CTAGAAAG 831
                                                                                                                                                                                          BG870337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                     DEFINITION
                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                 BG870337
                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                g
                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                         BG865768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qα
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                  /db_xref="taxon:10090"
/clone="IMAGE:4924056"
/clone="lnAGE:4924056"
/clone="ln="NoI_GGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/noLe="Organ: salivary gland; Wector: pCMV-SPORT6; Site_1: NoI: Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NOI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 CTGAATCTGGATGTGGATTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 ATTCTAGAAACGTTGAACACAGGGGACCTTGGCAATTTAAAAAGCTTTACATCT---TTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 GACATTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 AATGGTT!ATTGTCGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGGTAAGCTGTCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 GATGATGCCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 TCCAACGCCAATGCCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 CCCATCATIGGCCAGATIAICAACCIGAAAGCCTCCTIGGACCTCCTGACAGTCACA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 ACAGATAAAATCTCCATTTCCTTGTGGGGAAGACGATTACCCATCATCAACAGTATTCTG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 GAIGGIGICICIACCCICCIIACAAGIACATIGICAAACGICCIGCAAACIICCIAIGI 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 CCACTGATCCGCATCTTCATCCACTCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 TCAGAGTCACTTCTTGGTGAACTTGGCAGCGCTGTGAATAATTTGA------- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 CCAACCAGCATCTCCATTTCCTTGCTGGACAAACAGGCCAAATCATCAACAAGTTCGTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650 CCATIGCITCAGTACGTCCTCAGCACACTGAATCCAAGTGTACTTCAGGGTCTCCTCTT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            710 AATCTACTGGCCAGGACCAGGTAACAACTTTGCCTCTGAAGAGGAAGAACAGAAGGATGG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        800 ACTGIGGIGCATGCIGATTGGITCCCAGTGGCITGCCCCACCCCCTTATAGCATCTCCCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTGGGCTGTTGTGGCCTGCTCATTGGGAAC 88
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 192; DB 10; Length 910; 53.9%; Pred. No. 2.1e-40;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       =
=
=
                /organism="Mus musculus"
                                     /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _
_
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                   236 a
                                                                                                                                                                                                                                                                                                                                                                  Matches 467;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
source
                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
/clone_lib="NCI_CGAP_SG2"
/lab_host="DHIOB (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
Not!; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."

268 c 205 g 294 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                     BG865768 1039 bp mRNA linear EST 29-MAY-20 602784358Fl NC1_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910534 5′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Producement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM10811 row: c column: 15

High quality sequence stop: 832.
770 CACAACTCTTCTGGCTGGTTAATCTCCAGGGTTTCACCTTACTTCTGATGGCATTTCCTT 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1039)
NIH #MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 TCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 CCTGTTCTTCACGAGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 --------AAATICTGAATCCTCCCTCTGAAGCTGTCCTCAGAAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 CTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 CTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTGGCCATTAGCCAAGAACAGC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 GCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ATTCTAGAAACGTTGAACACGGGGCCTTGGCAATTTAAAAAGCTTTACATCT---TTG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 AGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 AAACCAAAGATGTTCCAACTTGGGAGCCTTGTTGTTGTGTGGGCCTGCTCATTGGGAAC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.7e-40;
0; Mismatches 369; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 1039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%; Score 191.2; DB 1 55.1%; Pred. No. 3.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:4910534"
                                                                      880 CCAGGAAGCTGCTGCCACCTAAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                         830 CTACAAAGTGGCAACTTTCATCACAC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG865768.1 GI:14216308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 55.19 tes 505; Conservative
                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG865768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
                                                                                                                                                                                                                                                                                                             BG865768
```

Q

ô q ò q

QQ

ò g ò

ô

pp

q

ò

ò q ò

```
EST 29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG868020 889 bp mRNA linear EST 29-MAY-20
602788382F1 NC1_CGAP_SG2 Mus musculus cDNA cLone JMAGE:4919756 5
                                                                                                                                                                                                        405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               705
GACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATC 399
                                                                 286 AATGGTTTATTGTTGAAAATCAATAATCTCAAAGTCCTGGATTTTCAAGCTAAGCTGTCT 345
                                                                                                                                                                                                                                                                      460 CCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACA 519
                                                                                                                                                                                                                                                                                                                                        406 CCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGACCTCATAAATTCACTCTCC 465
                                                                                                                                                                                                                                                                                                                                                                                                      520 ATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGAC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 ATTAAAACCAATGCCCAGACTGCCTTCCTGAGGTGACCATAGGCAAATGCTCCAGTAAT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 AATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           700 CCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCACCAGAAGGACC 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  824 TCTTAGAAAGTIGT-ACTTATCATCCCACATTTCTACCTGAGACCAACCCAAAGGAGC 882
                                                                                                                                   400 GATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGGGAATGTCACTGTGGCCGGG
                                                                                                                                                                                                 TCCAACGCCAATGGCATTGATCTGACGGTGCCCTTGGCTGGGGAAGCCTCCTTGGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 CCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGGCCAAATCATCAACAAGTTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 ACAGATAAAATCTCCATTTCCTTGINGGGAAGACGATTACCCATCATCAACAGTATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 CCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGTTCTTCAGGTTCTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 AATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAA-TGAGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCTACTTTGCAGGA--CAGGTACAACTTGCCCTCTGAAGAGGACGAACAGAAGGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 CACAATCTTCCTGTCTGGATACTCTCCAGGGTTTCATCTTACTTCTGATGGGCATTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =
=
=
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10835 row: c column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG868020.1 GI:14218560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       939 TICCCAGAIACCCCIIC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 CITCCAGAATICTCTTC 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BG868020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG868020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
```

q

g

ŏ

δ q

```
500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 TAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 TGAAGCTGTCCCTCAGAACCTGAATCTGGATGTGGAGTTGCTTCAGCAAGCCACAAGTTG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 GCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 GCCATTAGCCAAGAACAGCATTCTAGAAACGTTGAACACAGCGGACCTTGGCAATTTAAA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 GCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 TGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 TITTCAAGCTAAGCTGTCTTCCAACGCCAATGGCATTGATCTGACGGTGCCCTTGGCTGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 GGAAGCCTCCTTGGTTCTGCCTTTCATTGGCAAGACGGTCGACATTTCTGTTTCCTTGGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 CCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCAGCGTGTTGCCGTCCT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 GGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 AATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 CATCATCAACAGTATTCTGGATGGTGTCTCTACCCTTACAAGTACATTGTCAACGT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 GCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 CCTGCAAAACTTCCTATGTCCATTGCTTCAGTACGTCCTCAGCACACTGAATCCAAGTGT 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   741 CATTCAGCAGGTCGTCGATAATC -- CTCAGCACAAACCCAGCTGCAAACCCTCATTTGA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 TCTTCAGGGTCTCCTCTTAATCTACTTGGCAGGACACGGTACAACTTGCCCTCTGAAGA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799 AGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 GGAAGAACCAGAAGGATGCCACAAATTCTCCTGCTGGGCTACTCTCCAGTGGTTTCATCT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      859 ACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  753 TACTTCTGATGGCATTTCCCTCTAGAAAGTGCT---ACTAATCATCCAGAATTTCTACC 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AAGCTTTACATCTTTGAATGGTTTATT --- GTTGAAAATCAATAATCTCAAAGTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 GAATGTCACTGTGGCCGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGA
                                                                                                                                                                                                                                                                                                                                                                        18.6%; Score 190.8; DB 10; Length 889; nlarity 55.7%; Pred. No. 4.3e-40; Conservative 0; Mismatches 332; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919 TGAGICCCACCAGAAGGACCIICCCAGAIACCCCIITCICCICACAGIC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism*"Mus musculus"
                                                                                         /db_xref="taxon:10090"
Location/Qualifiers
                                                                     /strain-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 428; Conserv
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                           source
                                                                                                                                                                                                                                                                              BASE COUNT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

Search completed: August 6, 2002, 16:52:39 Job time: 10146 sec

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Database :

Expressed sequence Expressed sequence Human secreted pro

Human digestive sy brain expres

foetal liver

Human foetal liver Human brain expres

marrow

Human bone

Probe #21962 used

Human brain expres Human bone marrow Probe #8883 used t

Expressed sequence

Expressed sequence Expressed sequence Human digestive sy Expressed sequence Human LUNX cDNA. LSITO gene derived Human LUNX cDNA.

LS170 gene consens Human DNA encoding

pro

secreted

Human

Human cDNA encodin polynucleoti polynucleoti digestive sy digestive sy

polynucleoti

Human Human

Нишап Human Human Human Human secreted pro MSRV-1 clone 8 pol

glutamicum codin

polynucleoti polynucleoti

Нишап

```
Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human parotid secretory protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                              AA153276
AAV44766
AAV44767
                                                                                                                                                                                                                                                                                                                            ABA90906
AAI58877
AAI60663
                                                                                                                           ABA72852
                                                                                                                                       AAK21285
                                                                                                                                                                                                                                         AAX00808
                                                                                                                                                                                                                                                                 AAZ61165
                                                                                                                                                                                                                                                                             AAX00809
                                                                                                                                                                                                                                                                                                                                                                 AAK87982
                                                                                                                                                                                                                                                                                                                                                                                                                  AAD05509
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH68310
                                                  AAA61274
                                                                                                                                                                                                    AAK87987
                                                                                                                                                                                                                                                                                                                                                                                                                               AAV43243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
49..798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV44759 standard; DNA; 1028 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= hPSP
49..102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US23522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag* b
                                  therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
12.
                                                 16.
16.
16.
16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09828420-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                        39
39
38.6
38.6
303.6
302.4
258.8
229.8
191
                                                            AAV44759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4AV44759
 U
                                                                                                                                                                                                                                                                                                                                                                                                     υυ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (without alignments)
8478.590 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human parotid secr
Human secreted pro
cDNA encoding huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein enco
Human PRO1025 nucl
Human parotid secr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence
Expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                       | Sidestage | State | 
                                                                                                                                                              1 CACGAGATTTCATGAGCATC.....AAGGCCCATTTCTGCAAAA 1028
                                                                                    August 6, 2002, 16:18:33 ; Search time 208.17 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV44759
AAA87727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV44760
AAV44761
AAV44762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH99686
AAC58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF64009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV37699
                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_032802:*
                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
                                                                                                                                   US-10-020-139-1
1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                         Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1041
1049
824
```

96US-0034429.

23-DEC-1996;

Score 1028

. 9

1019.8 1019.8 994.4 990.4 818.4 383.8 374.8

```
those characterised by overexpression and/or activation of the amplified antibodies. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., remal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, all lypothalamic and other glandlar, macrophagal, epithelial, strongal, hypothalamic and other glandlar, macrophagal, angiogenic and immunologic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC5836 represent pcR primers and hybridisation probes used in the isolation of the human pRO sequences. AAC58367 to AAC58367 in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
```

Sequence 1049 BP; 279.A; 299 C; 236 G; 235 T; 0 other;

```
0
                                                                                                                                                         223 ggcatccttgagaaactgaaggtcgacctaggagtgcttcagaaatccagtgcttggcaa 282
                                                                                                                                                                                                                                                                                                                                                                   43 totgaggtggtggtcaagacaaaagatgcttcagctttggaaacttgttctcctgtgcggc 102
                                                                                                                                        85 GTGCTCACTGGGACCTCAGAGTCTCTTGACAATCTTGGCAATGACCTAAGCAATGTC 144
                                                                                                                                                                                                        145 GTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAA 204
                                                                                                                                                                                                                                                                         205 GGCATCCTTGAGAAGCTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 AAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAAT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 aaagetgaacegalegatgatgaeggeaaaggeettaaeetgagetteeetgteaeegegaat 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 CTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                   325 CTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAACTGGCTCATCCTGGATGTC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 GTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTGCTTGGACCTC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 CTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCCAGCCTGTTGCCGTCCTGGGA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 gaatgegecagtgacccaaccagcateteaettteettgetggacaaacacagecaaate 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 GAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 ATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 atcaacaagttcgtgaatagcgtgatcaacacgctgaaaagcactgtatcctccctgctg 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAGGAGATAIGICCACTGATCCGCATCTTCATCCACTCCTGGATGTGAATGTCATT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 CAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                   25 TCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGC 84
96.3%; Score 990.4; DB 21; Length 1049; 99.4%; Pred. No. 6.3e-290;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
9
                                   0; Mismatches
                                   Matches 994; Conservative
                    Best Local Similarity
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685
                                                                                                    qq
                                                                     ò
                                                                                                                                                                    Q
                                                                                                                                                                                                                                       q
                                                                                                                                        õ
                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                            QC
                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
that bind specifically to, and modulate activity of HSSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, or care disease, thyroiditis, insulin-dependent diabetes, pancreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HSSP nucleic acid are used to produce recombinant HSSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HBSP-expressing cells, to detect cells
                                                                                                                                                                      Parotid secretory protein; human; cancer; autoimmune disease; secretory lissue; asstrointestinal tissue; HSPSP; Syorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA encodes a human parotid secretory protein (HPSP). Antagonists
805 CGAATGAGGAGGACCACTGTGGTGCATGCTTGGTTCCCAGTGGCTTGCCCCACCCCC 864
                                      823 cgaatgaggaggaccactgtggtgcatgctgattggttcccagtggcttgccccacccc 882
                                                                          865 TTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTC 924
                                                                                                              883 ttatagcatctccctccaggaagctgccaccacctaaccagcgtgaaagcctgagtc 942
                                                                                                                                                  925 CCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACA 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New parotid secretory protein - useful for, e.g. treatment of cancer and auto-immune disease, particularly of secretory or gastrointestinal tissues
                    /product= "parotid secretory protein"
/note= "#"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human parotid secretory protein (HPSP) encoding DNA.
                                                                                                                                                                                                                          985 CATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTCTGCA 1024
                                                                                                                                                                                                                                                                1003 catgttgtcctgccctggcaataaaggcccatttctgca 1042
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 1A-C; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAV37699 standard; DNA; 824 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US20651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0749288.
                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WP1; 1998-297933/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW60682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9821329-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                              AAV37699;
                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                          δà
                                                                                                            G
                                                                                                                                                  ò
                                                                                                                                                                                      a
                                                                                                                                                                                                                            òγ
```

AAV44760 standard; DNA; 449 BP

```
ö
                    purification of HPSP from natural sources. Expression of HPSP may indicate call proliferation. HPSP nucleic acid or its fragments are used to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease,
  that express HPSP, to monitor patients being treated with HPSP, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                 66 ACTIGITCICCIGICCGCGCGTCCTCACTGGGACCTCAGAGTCTCTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 CANTGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 agttgacaatantettaaaggeateettgagaaactgaaggtegaeetaggagtgettea 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGGCCCAGGAAGCTGAGAAATTGCTGAAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 caatgacctaaqcaatgtcgtggataagctggaacctgttcttcacgagggacttgagac 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCCAGATTATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCA 545
                                                                                                                                                                                                                                                                                                                                                              65 actigiteteciglyeggegigeteacigggaeeteagagietetietigaeaateiigg 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 caatgicattictaagcigcticcaactaacacggacattitigggitgaaaatcagcaa 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 cttccctgtcaccgcgaatgtcactgtggccgggcccatcattggccagattatcaacct 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 gaaagceteettggaceteetgacegeagteacaattgaaactgateeceagacacaee 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 GCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 geotyttgeegteetgggagaatgegeeagtgaeeeaaeeageateteaettteettget 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 ggacaaacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaag 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 CACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 cactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatccactc 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726 CCTGGATGTGAATGTCATTCAGCAGGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725 cctggatgtgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgca 784
                                                                                                                                                                                                                                                                                                                                  6 GATTICATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ACTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                  Sequence 824 BP; 226 A; 225 C; 184 G; 189 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 818.4; DB 19;
Pred. No. 8.3e-238;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 AACCCICATITGAAGAGGACGAATGAGGAGGACCACIGIG 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              785 aacceteatetgaagaaggaegaatgaggaggaeetgtg 824
                                                                                          by hybridisation, particularly for diagnosis an
but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                79.6%; Scur-
99.9%; Pred
0; h
                                                                                                                                                                                                                                                               Best Local Similarity 99.9
Matches 819; Conservative
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486
0000000x8
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

RESULT AAV44760

```
DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention. The DNA of the invention of the invention of the corresponding useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immuno defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                   Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TGGAAACTIGITCTCCTGTGCGGGGGGGCTGGGACCTCAGAGGTCTTCTTGACAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 tggaaacttgttctcctgtgcggcgtgctcactgggacctcagagtctcttcttgacaat 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttygcaatgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggactt 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CACGAGATITCAIGAGCAICCICCICIAAACGCGIGICAAGACAAAAGAIGCIICAGCII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 cacgagatttcatgagcatcctcctctaaacgcgtgtcaagacaaaagatgcttcagctt 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an expressed sequence tag with homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.3%; Score 383.8; DB 19; Length 449; 95.5%; Pred. No. 4.3e-106; Live 0; Mismatches 11; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 449 BP; 122 A; 107 C; 106 G; 110 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 75-76; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to identify hPSP-binding proteins.
                                                                                                                              Expressed sequence tay HSGSA61R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0034429.
                                                                                  16-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 427; Conservative
                                                                                                                                                                                                                 therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                    W09828420-A1
                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                             02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Op
```

```
This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (anti)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                     AGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGA 293
                                                                                                                      243 aggagtgetteayaaateeagtgettggeaaetggeeaageaggaeggeeeaggaagetga 302
                                                                                                                                                              294 GAAATTGCTGAA-CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGT 352
                                                                                                                                                                                    363 igaaaaaicagcaacicceicaicciggaigteaaagcigaaccgaicgaigaiggnaaa 422
181 GAGACAGTTGACAATACTCTTAAAGG------CATCCTTGAGAAACTGAAGGTCGACCT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                            412 GGCCTTAACCTGAGCTTCCCTGTCACC 438
                                                                                                                                                                                                                                                                                                                                                                 423 ggettaaactggagetteectgteane 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 76; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag HSGSC13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV44761 standard; DNA; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US23522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0034429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duan R, Ruben SM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09828420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV44761;
                                                                                                                                                                                                       303
                                                                                                                    Q<sub>O</sub>
                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                 QQ
                                       g
                                                                                                                                                            ô
                                                                                                                                                                                                 q
                                                                                                                                                                                                                                             δŏ
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
ģ
the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                              71 TTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGGCAATG 130
                                                                                                                                                                                                                                                                                                                                                                                              191 ACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAAAT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 acaatactcttaaaggcatccttgagaaactgaaggtcgacctaggagtgcttcagaaat 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAAAATG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 TCATTICTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAACTCCC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 tecetgiteacegggaaigiteaanginggeeegggeeenteatigggeeagnitateaa 479
                                                                                                                                                                                                                                                                                                                                 61 ttctcctgtgcggcgtgctcactgggacctcagagtctcttcttgacaatcttggcaatg 120
                                                                                                                                                                                                                                                                                                                                                                         131 ACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGTTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ccagigettggcaactggccaa.cagaaggnccaggaagetgagaaattgetgaacaatg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 TCATCCTGGATGTCAAAGCTGAACCGATGATGGCAAAGGCCTTAACC----TGAGC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 ncanccggatgttcaaagntgnancgatcgatgatgggcaaaggctttaanccggaggct 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 TTCCCTGTCACCGCGAATGT---CACTGTGGCCGGGCCCATCATT-GGCCAGATTATCAA 482
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                  12 ATGAGCATCCTCTAAAACGCGTGTCAAAAAAAAAGATGCT-TCAGCTTTGGAAACTTG 70
                                                                                                                                                                                                                                                      1 atyagnatectectetaaaegegtyteaagaeaaaagatgetnneagetttggaaaettg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 -- CCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.5%; Score 374.8; DB 19; Length 538; 87.7%; Pred. No. 2.5e-103; Live 0; Mismatches 54; Indels 12;
                                                                             Sequence 538 BP; 140 A; 126 C; 128 G; 124 T; 20 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag HSGSA89R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0034429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US23522,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV44762 standard; DNA; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1998 (first entry)
                                                                                                                                                      Best Local Similarity 87.79
Matches 469; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV44762;
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV44762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                 Dp
  S \times S \times S
                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
This sequence represents an expressed sequence tag with homology to the DNA of the invertion, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention accordes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immune assays), particularly system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparastic and antiviral agents and may be expressed in vivo from the DNA. The protein or cells expressing it are used in screening tests to identify specific acids, which are potentially useful for treating antisense nucleic acids, which are potentially useful for treating the containing the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                                                               New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 76-77; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to identify hPSP-binding proteins.
                                                                                                                               WPI; 1998-377651/32.
                                               Duan R, Ruben SM;
```

61 TGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTGACAAT 120 121 CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCT-GGAACCTGTTCTTCACGAGGGACT 179 183 tgagacagttgacaatactcttaaaggcatccttgagaaactgaggtcganclaggagt, 242 63 tggaaacttgttctcctgtgcggcgtgctcactgggacctcagagtctcttcttgacaat 122 123 ottggcaatgacctaagcaatgtcgtggataagctgggaacctgttctcacgagggact 182 180 TGAGGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGAGCTAGGAGT 239 240 GCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGG-CCCAGGAAGCTGAGAAAT 298 3; .Gaps 1 CACGAGATITCAIGAGCATCCTCTCTAAACGCGTGTCAAGACAAAAGAIGCTICAGCTI 60 3 cacgagatttcatgagcatcctcttaaacgcgtytcaagacaaaagatgcttcagctt 62 303 tgctggancaatgtcaattctaagctgnttccgactaacacggncatttttgggttg 359 299 TGCT-GAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTG 354 Score 312.8; DB 19; Length 359; Pred. No. 1.3e-84; 0; Mismatches 7; Indels 3; 0; Mismatches Query Match Best Local Similarity 97.28; 347; Conservative Matches g ά g ò q q à qq à ò

.,

Sequence 359 BP; 94 A; 79 C; 90 G; 90 T; 6 other;

```
Expressed sequence tag HSPAI14R.
                                    AAV44763 standard; DNA; 374 BP
                                                                                                            16-OCT-1998 (first entry)
                                                                        AAV44763;
10
                AAV44763
```

```
This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parctic secretory protein (HPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of HPSP (in standard blotting, amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune salvard gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparastic and antiviral agents and may be expressed in vivo from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive PSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 374 BP; 86 A; 123 C; 82 G; 78 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 77; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                        97WO-US23522.
                                            therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                         Duan R, Ruben SM;
                                                                                           Homo sapiens.
                                                                                                                                                                                                                        18-DEC-1997;
                                                                                                                                                                                                                                                                  23-DEC-1996;
                                                                                                                                                                           02-JUL-1998.
```

```
644 GCGTGATCAACACCGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCAC 703
                                                                                                                                                                                                              704 TGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 763
                                                                                                                                                                                                                                                                  74 tgatccgcatcttcatccactccctggatgtgaatgtcattcagcaggtcgtcgataatc 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 CTCAGCACAAAACCCAGCTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTG 823
                                                                                                                                                                                                                                                                                                                                                                               134 ctcagcacaaaacccagctgcaaaccctcatctgaagaggacgaatgaggaggaccactg 193
                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCT-GAGTCCCACCAGAAGGACCTTCC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                          14 gcgtgatcaacacgctgaaaagcactgtatcctcctgctgcagaaggagatatgtccac 73
29.5%; Score 303.6; DB 19; Length 374; 95.0%; Pred. No. 8.3e-82;
                                                         14; Indels
                                                         Mismatches
                                                      .;
                                                   Matches 343; Conservative
                            Local Similarity
  Query Match
```

g

g ò q

δ

```
The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oliqo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be sed to be a contained from mRNAS with intext 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in the contained.
                                                                                                                                                                                                                                                                                                                                                           Human, 5' EST; expressed sequence tag; secreted protein, cDNA isolation, gene therapy, chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic, forensic, gene therapy and chromosome mapping procedures -
943 CAGATACCCC-TICTCCTCACAGTCAGAACAGCAG--CCTCTACACATGTTGTCCTGCCC 999
                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 27560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 27560; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression and secretion vectors.
                                                                                                                                                                                                            AAC23485 standard; cDNA; 317 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                        06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                           1000 C 1000
                                                                                                                374 C 374
                                                                                                                                                                                                                                                 AAC23485;
                                                                                                                                                                                            AAC23485
                                                                                                                                                                         RESULT
  ô
                                    q
                                                                           ò
                                                                                                                Q
D
```

```
;
0
                                                                                                                                                                 617 GCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCT 676
                                                                                                                                                                                                                                                             677 CCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGA 736
                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                  1 gccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaagcactgtatcct 60
                                                                     29.4%; Score 302.4; DB 21; Length 317; 99.7%; Pred. No. 1.8e-81; tive 0; Mismatches 1; Indels 0;
Sequence 317 BP; 82 A; 100 C; 68 G; 67 T; 0 other;
                                                                                                                     Conservative
                                                                                            Similarity
                                                                                                 Best Local Sim
Matches 303;
                                                                       Query Match
```

```
This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application for immune salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and entisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to identify becoming the protein and chistor and particular and may be protein and this can be used to chaster Ab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parotid secretory protein; hPSP; digestive disorder; endocrine disorder;
                       797 GAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCC 856
                                                                                                                               181 gaagaagaacgaatgaggaaggaccactgtggtgcatgctgattggttcccagtggcttgcc 240
                                                                                                                                                                         857 CCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCCTAACCAGCGTGAAAG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-immune defensive disorder; immune system disorder; cancer; human;
737 ATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCCTCATTT 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 77; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to raise Ab, useful for diagnosis, to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag HSGSC78R.
                                                                                                                                                                                                                                                                                                                                                                                                               AAV44764 standard; DNA; 406 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0034429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US23522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duan R, Ruben SM;
                                                                                                                                                                                                                                                             917 CCTG 920
                                                                                                                                                                                                                                                                                                       301 cctg 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9828420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV44764;
                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                               AAV44764
                                       q
                                                                                     δ
                                                                                                                             q
                                                                                                                                                                         ò
                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                             òχ
```

X S

ô g ô g ò g à

```
AAA61274;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA612
000000000000000x0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                120 tgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagacagt 179
                                                                                                                                                                                                                                                                                                                                                                                        189 TGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 ATCCAGTGCTTGGCAACTGGCCAAGCAGGCCC---AGGAAGCTGAGAATTGCTG-- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 atccagtgcttggcaactgggccancagaaaggcccagggaaagcggagaaattgctgga 299
                                                                                                                                                                                                                                69 IGTICTCCTGTGCGGGGGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGGCAA 128
                                                                                                                                                                                                                                                                   60 tgttctcctgtycggcgtgctcactgggacctcagagtctcttcttgacaatcttggcaa 119
                                                                                                                                                                                                                                                                                                             129 TGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                           180 tgacaatactettaaagyeateettgagaaaetgaaggtegaeetaggagtgetteagaa 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an expressed sequence tag with homology to to DNA of the invention, and its all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The HPSP DNA is
                                                                                                                                                     9 TTCATGAGCATCCTCTTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACT 68
                                                                                                                                                                                          1 ttcatgagcatcctcctctaaacgcgtgtcaagacaaaagatgcttca-ctttggaaact 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                     ..
œ
                                                                                                                                                                                                                                                                                                                                    DB 19; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 -- AACAAIGICAITICIAAGCIGCTICCAACIAACACGGACATITITIGGG 351
                                                                                                                Indels
                Sequence 406 BP; 110 A; 95 C; 95 G; 100 T; 6 other;
                                                                      25.2%; Score 258.8; DB 1
89.4%; Pred. No. 3.4e-68;
live 0; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 78; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tag HSPMD56R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV44765 standard; DNA; 493 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0034429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US23522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-1998 (first entry)
                                                                                             Best Local Similarity 89.4°
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9828420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV44765;
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV44765
```

QQ

g

δ

```
useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                          DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant) agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 TGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 aaagcactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatcc 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 actecetggatgtgaatgteatteageaggtegtegataateeteageacaaaaceeage 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782 TGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 AAAGCACTGTATCCTCCCTGCTGCAGGAAGGAGATATGTCCACTGATCCGCATCTTCATCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      722 ACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; AIDS; autoimmune disorder; allergy; cardiovascular; viral; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%; Score 229.8; DB 19; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Florence KA, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 493 BP; 118 A; 143 C; 107 G; 122 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.3e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein gene 15 clone HSPBY40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.4%; Pred. w...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal infection; immunosuppressive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ni J, Ruben SM, Rosen CA, Ebner R,
Birse CE, Carter KC, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA61274 standard; DNA; 653 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0108207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US26409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        842 TCCCAGTGGCTTGCCCC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 agccagtctctgtgccc 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200029422-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000.
```

ö

```
2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-58PP-2000
06-58PP-2000
06-58PP-2000
08-58PP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                             14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-SEP-2000;
                                                                                                                                                                                                                                                                                                                14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
                                                                                                                                                          28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                    14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-2000;
The given relates the secret of the clone it was derived from are given in the descriptor line.

The invention relates to 31 novel genes and the clone it was derived from are given in the descriptor line.

The invention relates to 31 novel genes and their fragments (nucleic acid sequences: AAAG1260-A61293, amino acid sequences AAAG1260-A61293, amino acid sequences AAAG1260-A61293, amino acid sequences AAAG1260-A61293, treating or ameliorating medical acid sequences: a. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides. Specific uses are described for each of the 31 polynucleotides. Specific uses are described for each of the 31 and include products for the diagnosis or treatment of cancer, tumours, AIDS, autoimmune disorders, allergy, cardiovascular disorders, viral, bacterial and fungal infection. The genes are used to generate fusion proteins by linking to the gene a human immunoglobulin portion (AAAG1251) for increasing stability of the fused protein as compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                         The present sequence represents a nucleic acid molecule which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 ctccaggaagctgctgccaccacctaaccagcgtgaaagcctgagtcccaccagaaggac 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 CTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACACACATGTTGTCCTGC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 CCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 ceetiggieteattecagaitggiteceagiggetigeeecaeeecettatageatetee 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878 CTCCAGGAAGCT4CTGCCACCACCTAACCAGCGTGAAGCCTGAGTCCCACCAGAAGGAC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 10; Indels 0; Gaps
                                                 Novel human secreted proteins useful for diagnosing, preventing, treating and ameliorating a medical condition e.g. cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human digestive system antigen genomic sequence SEQ ID NO: 3374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 18.6%; Score 191; DB 21; Length 653; Local Similarity 95.2%; Pred. No. 1.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 653 BP; 156 A; 193 C; 152 G; 151 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            998 CCCIGGCAATAAAGGCCCATTTCTGCA 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 238; 295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK89798 standard; DNA; 7524 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein only.
                 WPI; 2000-387729/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK89798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                        disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK89798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
```

qq δ ò

```
2000US-0229345.
2000US-0229509.
2000US-0229513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0233063.
2000US-0233064.
2000US-0233065.
                           20000S-0225758.
2000US-0225759.
                                                                                                                                                                 2000US-0229343.
2000US-0229344.
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0232399.
2000US-0232400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0234223.
2000US-0234274.
2000US-0225447
2000US-0225757
                                                                          20000US-0226681
                                                                                         20000S-0226868
                                                                                                                                     2000US-0228924
                                                                                                                                                    2000US-0229287
                                                                                                                                                                                                                                                                                                                                                                                 2000US-0231968
                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0232398
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0232401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0236802
                                                                                                                                                                                                                                                                                                                                                                  2000US-0232081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0234997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20000US-0235834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000; 29-SEP-2000; 02-OCT-2000;
```

2000US-0237037

```
Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0249215.
2000US-0249216.
2000US-0249217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0250391,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0246532.
2000US-0246609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0249210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249265.
2000US-0249297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0250160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0251030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251989.
2000US-0251990.
                                                      2000US-0237039
                                                                              2000US-0237040
2000US-0239935
                                                                                                                                                                                                                                                                                                               2000US-0241808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0246523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0246528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0246610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0246611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0246613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0249208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0249211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0249214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20000US-0249245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0256719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0251479,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2001; 2001US-0259678.
                                                                                                                                        2000US-0239937
                                                                                                                                                                                                                                                                                                                                          2000US-0241809
                                                                                                                                                                                                                                                                                                                                                                  20000S-0241826
                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0244617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000015-0246476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0246478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0246525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0246527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0249207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20000S-0249244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0251988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0251856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-502630/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 - NOV - 2000; 2 17 - NOV - 20
                                                                           13 - CCT - 2000;
13 - CCT - 2000;
20 - C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOV-2000;
NOV-2000;
NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2
01-DEC-2
01-DEC-2
05-DEC-2
```

```
963 gigicaagacaaaagaigeticagetitiggaaactigtieteetgigegegigeteeteaet 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1023 gggacctcagagtctcttcttgacaatcttggcaatgacctaagcaatgtcgtggataag 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 GGGACCTCAGAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAG 153
                                                                           The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 CTGGAACCTGTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCA 208
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.9%; Score 173.4; DB 22; Length 7524; Best Local Similarity 99.4%; Pred. No. 1.3e-41; Matches 174; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                         Sequence 7524 BP; 2170 A; 1586 C; 1582 G; 2186 T; 0 other;
                        Disclosure; SEQ 1D NO 3374; 986pp; English.
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
```

ô

Search completed: August 6, 2002, 17:28:16 Job time: 4183 sec

Wed Aug 7 05:46:08 2002

```
(without alignments) 7731.369 Million cell updates/sec
                                                                                                                                                                                                                                                                      1 CACGAGATTTCATGAGCATC......AAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                    August 6, 2002, 16:25:18 ; Search time 2876.68 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                     43959072
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     21979536 segs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                                                                                                                      US-10-020-139-1
1028
                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                         OM nucleic
                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                    Run on:
```

Database :

```
414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                               Res
                                                                                                                                                                                                                                              /ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US081_comB.seq:*
/ggn2_6/ptodata1/pna/US091_comB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pna/056001_coMB.seq.*
/cgn2_6/ptodata/1/pna/056002_coMB.seq:*
/cgn2_6/ptodata/1/pna/U56003_coMB.seq:*
/cgn2_6/ptodata/1/pna/U56004_coMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
Pending_Patents_NA_Main:*
// cgn2_6/ptcdate/1/pna/PCTUS_COMB.seq:*
// cgn2_6/ptcdate/1/pna/USO6_COMB.seq:*
// cgn2_6/ptcdate/1/pna/USO8_COMB.seq:*
// cgn2_6/ptcdate/1/pna/USO8_COMB.seq:*
// cgn2_6/ptcdata/1/pna/USO80_COMB.seq:*
// cgn2_6/ptcdata/1/pna/USO82_COMB.seq:*
// cgn2_6/ptcdata/1/pna/USO82_COMB.seq:*
// cgn2_6/ptcdata/1/pna/USO82_COMB.seq:*
```

```
/cgn2_6/ptodata/1/pna/US6005_COMB.seq:

/cgn2_6/ptodata/1/pna/US6006_COMB.seq:

/cgn2_6/ptodata/1/pna/US6008_COMB.seq:

/cgn2_6/ptodata/1/pna/US6008_COMB.seq:

/cgn2_6/ptodata/1/pna/US6010_COMB.seq:

/cgn2_6/ptodata/1/pna/US6011_COMB.seq:

                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/l/pna/US6022_COMB.seq:*
/cgn2_6/ptodata/l/pna/US6023_COMB.seq:*
/cgn2_6/ptodata/l/pna/US6024_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptcdata/1/pna/US6033_COMB.seq:*/cgn2_6/ptcdata/1/pna/US6034_cOMB.seq:*/cgn2_6/ptcdata/1/pna/US6035_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 374, Appli Sequence 2263, Appli Sequence 211 Appli Sequence 31384, Appli Sequence 3195, Appli Sequence 2764, Appli Sequence 2764, Appli Sequence 2764, Appli Sequence 2204, Appli Sequence 5582, Appli Sequence 5582, Appli Sequence 5582, Appli Sequence 2910, Appli Sequence 2910, Appli Sequence 2910, Appli Sequence 2911, Appli Sequence 95211, Appli Sequence 97422, Appli Sequence 97422, Appli
SUMMARIES	US-08-993-529-1 US-09-469-099-26 US-09-759-408-26 US-09-759-408-26 US-09-759-408-26 US-09-758-470-2563 US-09-756-170-2563 US-09-756-170-2563 US-09-756-170-2563 US-09-756-170-2563 US-09-756-170-2563 US-09-758-471-27-3095 US-09-758-471-27-27-4 US-09-758-471-27-27-4 US-09-758-472-173 US-09-758-472-173 US-09-758-472-173 US-09-726-170-1741 US-09-726-170-1742 US-09-933-524-95211 US-09-933-524-97422 US-09-933-524-97422 US-09-933-524-97422
DB	111020202111111040202020202011111041102020202
Length	10028 10028 10028 10028 10028 10028 1004 1004 1006 1006 1006 1008 1008 1008 1008 1008
% Query Match	0.000000000000000000000000000000000000
Score	01010101010101010101010101010101010101
esult No.	10 8 4 5 9 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

9 9 180

```
961 ACAGTCAGAACAGCAGCCTCTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTC 1020
                                                               TGGAAACTIGTTCTCCTGTGCGGCGTGCTCGCGGACCTCAGAGTCTCTTGACAAT 120
                                                                                                                                       CITCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAGGCCCAGGAAGCTGAGAAATTG 300
                                                                                                                                                                                                                                                                                                CTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATC 360
                                                                                                                                                                                                                                                                                                                                                        CTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 CACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 TIGCIGGACAAACACAGCCAAATCATCAAGAAGTTCGIGAATAGCGIGATCAACACGCTG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 AAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  721 CACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 CTGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841 ITCCCAGTGGCTTGCCCCCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCAC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                841 TICCCAGIGGCTIGCCCCACCCCCTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCAC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 CTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 CTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTC 960
                       1 CACGAGATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACACAAAAGATGCTTCAGCTT
      1 CACGAGATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTT
                                                                                                                        CITGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTT
                                                                                                                                                                                181 GAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 TGCAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 TGCAAAA 1028
                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                            ò
                                                                                                                                                 a
                                                                                                                                                                                ò
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
   Sequence 4862, Ap
Sequence 1332, Ap
Sequence 10989, A
Sequence 96481, A
Sequence 96481, A
Sequence 96481, A
Sequence 97559, A
Sequence 97559, A
                                                                                                                                              Sequence 551, App
Sequence 3212, App
Sequence 10, Appl
Sequence 43461, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
US-09-652-122-4862
US-09-293-972-10389
US-09-204-939-10389
US-09-904-93-10989
US-09-933-524-96481
US-09-933-524-96481
US-09-933-524-96481
US-09-933-524-96481
US-09-933-524-9559
US-09-933-524-97559
US-09-933-525-10
US-09-933-525-10
US-08-975-985-3212
US-08-975-985-3212
US-09-975-985-3212
US-09-975-985-3212
US-09-975-985-3212
US-09-975-985-3212
US-08-975-985-3212
US-08-975-985-3212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1028; DB 13; Best.wocal Similarity 100.0%; Pred. No. 1.3e-279; Matches 1028; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08993529
GENERAL INFORMATION:
PAPLICANT: DUAN, ROXANE
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: Parotid Secretory Protein
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMUNICATION INCORATION:
TELECOMUNICATION INCORATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
INFORMATION FOR SEC 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1028 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
103..795
   819
3398
3398
4462
4462
4493
4493
4493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49..795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , LOCATION:
US-08-993-529-1
                                                                                                                                                                                                                                                                                       US-08-993-529-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
   STATE:
```

Wed Aug

```
444 cttccctgtcaccgcgaatgtcactgtggccgggcccatcattggccagattatcaacct 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/599,360B CURRENT FILING DATE: 2000-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-12-22
PRIOR PELLING DATE: 1998-12-22
PRIOR PAPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Von Heijne matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09599360B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Bougueleret, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/113,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 67..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 67..813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1026 AAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 aaa 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-599-360B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                      Dβ
                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                 d
                                                                                                                           ò
                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                         APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET. 050AUS
CURRENT APPLICATION NUMBER: US/09/469,099
CURRENT FILING DATE: 1999-12-21
EARLIER FILING DATE: 1999-12-22
EARLIER FILING DATE: 1999-12-22
EARLIER FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PARENTE FILING DATE: 1999-06-25
SOFTWARE: PARENTE APPLICATION NUMBER: 60/141,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGCCCATCATTGGCCAGATTATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 acttgttetectetytgeggegtgeteactgggaeeteagagtetettettgaeaatettgg 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 caatyacctaagcaatgtcgtggataagctggaacctgttcttcacgaggacttgagac 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATCCAGTGCTTGGCAACTGGCCAAGCAGGCCCAGGAAGCTGAGAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 gaaatccagtgertggcaactggccaagcagaaggccagggaagetgagaaattgetgaa 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 caatgtcatttctaagctgcttccaactaacacggacatttttgggttgaaaatcagcaa 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATGATGATGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 gatttcatgagcatcctcctctaaacgcgtgacaagacaaaagatgcttcagctttggaa 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GATTTCATGAGCATCCTCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%; Score 1019.8; DB 18; Length 1058; 99.8%; Pred. No. 2.8e-277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: SCORE 5.20 OTHER INFORMATION: SEG QLWKLVLLCGVLT/GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 67..111
OTHER INFORMATION: Von Heijne matrix
                                      Sequence 26, Application US/09469099 GENERAL INFORMATION:
                                                                                 APPLICANT: Dumas Milne Edwards, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 99.8
Matches 1021; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: polyA_signal
LOCATION: 1023..1028
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                         APPLICANT: Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1042..1058
US-09-469-099-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 67..813
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                 1058
                        US-09-469-099-26
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
APPLICANT: Jobert, S. TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides FILE REFERENCE: GENSET.050CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966 CAGAACAGCAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                   906 CAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924 cagogigaaagooigagicocaccagaaggacoiicocagaiaccooiicocagaia
                                                                                                                                  546 GCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCT 605
                                                                                                                                                                 606 GGACAAACACGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG 665
                                                                                                                                                                                                                                                                                                726 CCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 AACCCICATITGAAGAGGACGAAIGAGGAGGACCACIGIGGIGCAIGCIGAIIGGIICCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           846 AGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 agiggetigececacecettatageatetecetecaggaagetgeegecaceacetaae 923
666 CACTGTATCCTCCCTGCTGCAGAAGAGATATGTCCACTGATCGTCGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 octggatgtgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgca 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 aacceteatetgaagaagaegaatgaggaggaceaetgtggtgeatgetgattggtteee 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: score 5.20
```

```
99.1%; Score 1018.4; DB 99.9%; Pred. No. 6.9e-277 tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PHO01
CURRENT APPLICATION NUMBER: US/09/758,472
                                                                                                                                                                                                                                                                                      ; Sequence 3794, Application US/09758472; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                           1026 AAA 1028
                                                                                                                                                                                     1044 aaa 1046
                                                                                                                                                                                                                                                                      US-09-758-472-3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-758-472-3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                           ò
                                                                                                   qq
                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                      ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTGTTCTCCTGTGCGGGGGGGGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                     84 acttgitciccigiqeggegigetecactgggaceteagagictetictigaeaatetigg 143
                                                                                                                                                                                                                                                                                                                                                                                                             126 CAATGACCTAAGCAATGTGGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 caatgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagac 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 agtigacaatacictiaaaaggcatccitgagaaacigaaaggicgacciaggagigcitca 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 gaaatccagtycttggcaactggccaagcagaaggcccaggaagctgagaaattgctgaa 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 CAATGICATITGIAAGCIGCTICCAACIAACAGGGACAIITITIGGGIIGAAAAICAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATGGTGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 ctccctcatcctggatgtcaaagctgaaccgatcgatgatggcaaaggccttaacctgag 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 ettecetgteaecgegaalgteaetgtggeegggeeeateattggeeagaltateaaeet 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 GCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 gootgilgeeqinotgagaaatgegeeagigaeeeaaooageateleettiootiget 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606 GGACAAACACGCCAAATCATCAACAAGTTCGTGAATAGCGTGAAGACACGCTGAAAAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624 ggacaaacacagccaaatcatcaacaagttcgtgaalaycqtgalcaacacgctgaaaay 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 CACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 cactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatccactc 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 cetggatgtgaatgtcattcaycaggtcgtcgataatcctcagcacaaaacccagctgca 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        786 AACCCICATITGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 aaccctcatctgaagaagacgaatgaggaggaccactgtggtgcatgctgattggttccc 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         846 AGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.54 agiggetigececaececettatageatetecetecaggaagetgetgecaecaectaae 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 CAGCGIGAAAGCCIGAGICCCACCAGAAGGACCITCCCCAGAIACCCCTICTCCTCACAGI 965
                                                                                                                                                                                                                                                                    6 GATTTCATGACCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 1058;
                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                  Pred. No. 2.8e-277
                                                                                                                                                          99.2%; Score 1019.8;
99.8%; Pred. No. 2.8e-
                                                                                                                                                                                                    0; Mismatches
OTHER INFORMATION: seq QLWKLVLLCGVLT/GT
                                                                                                                                                                                                      Conservative
                   NAME/KEY: polyA_signal LOCATION: 1023..1028
                                                       ) NAME/KEY: polyA_site
) LOCATION: 1042..1058
US-09-599-360B-26
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                    Matches 1021;
                                                                                                                                                                 Query Match
                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426
                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
966 CAGAACAGCAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                     924 cagogtgaaagcetgagteecaccagaaggaeetteecagataeeeetteteeteacagt 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 TGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTCTTGACAATCTTGGCAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 ATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAACAA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 tyltotootytyoogogtyotoactyggacotoagagtotottottgacaatottygoaa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 tgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagacagt 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 tyacaalaclottaaaggcatcottyagaaactgaaggtcgacotaggagtgottcagaa 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 atccagtgettggcaaettggccaagcagaaggeccaggaagetgagaaattgetgaacaa 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 IGTCATTICTAAGCIGCTICCAACTAACACGGACATTITIGGGTIGAAAATCAGCAACTC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 tgtcatttctaagctgcttccaactaacacggacatttttgggttgaaaatcagcaactc 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 CCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAAACCTGAGCTT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 cctcatcctggatgtcaaagctgaaccgatcgatgatggcaaaggccttaacctgagctt 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 CCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 occigicacogogaaigicacigiggocoggocoaicaitggocagaitaicaacoigaa 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 AGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCCAGACACCACCAGCC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ttcatgagcatcctcctctaaacgcgtgtcaagacaaaagatgcttcagctttggaaact 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TTCATGAGCATCCTCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 TGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAA
DB 29; Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: Indels
```

ö

```
g
                                                                                                           ò
                                                                                                                                                 QQ
                                                                                                                                                                                            ò
                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       969 AACAGCAGCCTCTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTCTGCAAAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 IGTIGCCGICCTGGGAGAAIGCGCCAGIGACCCAACCAGCAICTCACITICCTIGCIGGA 608
                                          552 tgttgccgtcctgggagaatgcgccagtgacccaaccagcatctcactttccttgctgga 611
                                                                                  609 CAAACACGCCAAATCATCAACATTCGTGAATAGCGTGATCAACACGCTGAAAAGCAC 668
                                                                                                                         612 caaacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaagcac 671
                                                                                                                                                                     669 TGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCT 728
                                                                                                                                                                                                            672 tgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatccactcct 731
                                                                                                                                                                                                                                                    729 GGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAAC 788
                                                                                                                                                                                                                                                                             789 CCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCACT 848
                                                                                                                                                                                                                                                                                                                                                                               792 octoatotgaagaggacgaatgaggaggaccaotgtggtgoatgotgattggttoocagt 851
                                                                                                                                                                                                                                                                                                                                                                                                                     849 GGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCACCTAACCAG 908
                                                                                                                                                                                                                                                                                                                                                                                                                                            909 CGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGTCAG 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               912 cgtgaaagcetgagteceaecagaaggacetteceagataceetteteeteaeagteag 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 acttgiticiccigigogggggggggctcactggggacctcagaggtctcttcttgacaatcttgg 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 caatgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagac 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AGTIGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ACTIGITOTOCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTCTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GATTICATGAGCAICCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 gatttcatgagcatcctctctaaacgcgtgtcaagacaaaagatgcttcagctttggaa 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%; Score 1018.2; DB 25; Length 1122; 99.7%; Pred. No. 8.1e-277; Live 0; Mismatches 3; Indels 0; 0
                                                                                                                                                                                            APPLICANT: Shyjan, Andrew W. TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR FILE REPERBAGE: 1600.1194-001 CURRENT APPLICATION NUMBER: US/09/652,122 CURRENT FILING DATE: 2000-08-30 PRIOR APPLICATION NUMBER: 60/151,421 PRIOR FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5020
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4943, Application US/09652122
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1020; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-652-122-4943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-652-122-4943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                         Dp
                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                  ò
                                                                                                                                                               ΩŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
966 CAGAACAGCAGCCTCTACACATGTTGTCGCCCCTGGCAATAAAGGCCCGTTTCTGCAA 1025
                                                                                                                                                                                                 246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                               306 CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 CTCCCTCATCCTGGATGTCAAAUCTGAACGGATGGATGATGATGAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 CTICCCTGTCACCGCGAATGICACTGTGGCCGGGCCCATCATTGGCCAGAITATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 agttgacaatactcttaaaggcatccttgagaaactgaaggtcgacctaggagtgcttca 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 caatgtcalltctaagctgcttccaactaacacggacatttttgggttgaaaatcagcaa 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 eteceteatectggatgteaaagetgaacegategatgatggeaaaggeettaacetgag 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 GAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 gaaageeteettggaeeteetgaeegeagteacaaattgaaactgateeecagaeaeaea 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 GCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 gectgitgeegteetgggaagaatgegeeagtgaeceaaeeageateteactiteettget 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 GGACAAACACACCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 ggacaaacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaag 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 CACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCGGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        698 cactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatccactc 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 CCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 cctggatgtgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgca 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        786 AACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 878 agtggcttgccccacccccttatagcatctccctccaggaagctgctgccaccacctaac 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 CAGCGIGAAAGCCIGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGT 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: OVCEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR THE OF INVENTION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/726,170
CURRENT FILING DATE: 2000-11.29
PRIOR APPLICATION NUMBER: 60/167,858
PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2263, Application US/09726170 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1026 AAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1058 ata 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-726-170-2263
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                               66 ACTIGITCICCIGIGGGGGGGGCTCACIGGGACCICAGAGICTCTICTIGACAAICIIGG 125
                                                                                                                                                                                                                                                                                                                                                                      126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 caatgacctaagcaatgtcgtggataagctggaacctgttcttcacgagggacttgagac 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 gaaatccagtgcttygcaactggccaagcagaaggcccaggaagctgagaaattgctgaa 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 CAATGTCATTTCTAAGCTGCTTCCAACTAACAGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 caatgtcatttctaagctgcttccaactaacacggacatttttgggttgaaaatcagcaa 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGGTGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 ctcoctcatcctggatgtcaaagctgaaccgatcgatgatggcaaaggccttaacctgag 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCCAGATTATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 GAAAGCCTCCTTGGACCTCCTGÄCGGCAGTCACAATTGAAACTGATCCCCAGACACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 gaaagceteettygaeeteetgaeegeagteacaattgaaaetgateeeeagaeacaeea 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 GGACAAACACAACCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 CACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 cactgtatcctccctgctgcagaaggagatatgtccactgatccgcatcttcatccactc 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 AACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 aaccctcatttgaagaggacgaatgaggaggaccactgtggtgcatgctgattgctccc 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 AGTGGCTTGCCCCACCCCCTTATAGCATCTCCCAGGAAGCTGCTGCCACCACCTAAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              878 agiggetigececaececetiatageatetecetecaggaageigetgeegeeceaectaae 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906 CAGCGIGAAAGCCIGAGICCCACCAGAAGGACCTICCCAGATACCCCTICTCCTCACAGI 965
                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                           6 GATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                     38 gatttcatgaycatcctctcaaacgcgtgtcaagacaaaagatgcttcagctttggaa 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 ACTIGACAATACTCTTAAAGGCATCCTIGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 cttccctgtcaccgcgaatgtcactgtggccgggcccatcattggccagattatcaacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 GCCTGTTGCCGTCCTGGAGAATGCGCCAGTGACCCAACCAGGATCTCACTTTCCTTGCT
                                                                                                                                                                     99.0%; Score 1018.2; DB 29; Length 1122; 99.7%; Pred. No. 8.1e-277; Live 0; Mismatches 3; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   Conservative
                                                                                 ; ORGANISM: Homo sapiens US-09-726-170-2263
                                                                                                                                                                                          Best Local Similarity
Matches 1020; Conserv
                                            1122
SOFTWARE: Fa:
SEQ ID NO 2263
                                                                 TYPE: DNA
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726
                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΟÝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
966 CAGAACAGCACCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                                                                     938 cagogtigaaagootigagicocaccagaaagacoticocagaiacootitotootoacagi 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTGTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 acttgttctcctgtgcggcgtgctcactgggacctcagagtctcttcttgacaatcttgg 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 agttgacaatactcttaaaggcatccttgagaaactgaaggtcgacctaggagtgcttca 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaaatccagtgcttggcaactggccaagcagaaggcccaggaagctgagaaattgctgaa 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 CAATGICATITCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 ctocctcatoctggatgtcaaagctgaaccgatcgatgatggcaaaggccttaacctgag 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 GAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCCAGATTATCAACCT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttccctgtcaccgcgaatgtcactgtggccgggcccatcattggccagattatcaacct 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GATTICATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 gatttcatgagcatcctcctctaaacgcgtgtcaagacaaaagatgcttcagctttggaa 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%; Score 1018.2; DB 29; Length 1122; 99.7%; Pred. No. 8.1e-277; tive 0; Mismatches 3; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gearing, David P.
APPLICANT: Fraser, Christopher C.
APPLICANT: Donovan, Michael J.
APPLICANT: Holtzman Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/726,175
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,859
PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                  Sequence 2853, Application US/09726175 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1600.2054-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1020; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                        1026 AAA 1028
                                                                                                                                                                                                    1058 ata 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-726-175-2853
                                                                                                                                                                                                                                                                                       US-09-726-175-2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278
                                                             ô
                                                                                                           a
                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ö

us-10-020-139-1.rnpm

```
970 teagaacageageetetacacatgttgteetgeeeetggcaataaaggeeeatttetgea 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            965 TCAGAACAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCA 1024
                               126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                       190 agttgacaatactettaaaaggeateettgagaaaetgaaggtegaeetaggagtgettea 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 GCACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         845 CAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAA 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAAC-C 484
                                                                                                                                               186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA
                                                                                                                                                                                                                                                                                                                                       cttccctgtcaccgcgaatgtcactgaggccgggcccatcattgaccagattatcaacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 ACCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 tggacaaacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790 aaacceteatetgaagaagaagaatgaggaggaccaetgtggtgcatgetgattggttee
                                                                                                                                                                                                                                                                                               GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 caatgicattictaagetgetteeaactaacaeggaeattittggggttgaaaateageaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 eteceteateetggatgteaaagetgaacegategatgatggeaaaggeettaaeetgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 TGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgagageeteettggaeeteetgaeegeagteacaattgaaaetgateeeeagaeaeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 geactgtatectecetgetgeagaaggagatatgteeactgateegeatetteateeact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 CCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             785 AAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caging the contraction of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         905 CCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 ccagcgtgaaagcctgagtcccaccagaaggaccttcccagatacccttctcctcacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Contigs Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3095, Application US/09471275; GENERAL INFORMATION: APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1025 AAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1030 ccaa 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-471-275-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                       Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 CAGAACAGCCACTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTCTGCAA 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          998 cagaacagcagcetctacacatgttgtcctgcccctggcaataaaggcccatttttgcag 1057
                                                                                                                                                                                                                                                               999
                                                                                                                                                                                                                                                                                                                                                                                                           725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ACTIGITCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTGTTGACAATCTTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 GCCTGTTCCCTCGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGCT 605
                                                                                                                                                                                   578 geetgitgengleetgggagaatgegecagigaeeecaaeeageaicteaetiteetigei 637
                                                                                                                                                                                                                                                                                                                                   638 ggacaaacacagccaaatcatcaacaayttcgtgaatagcgtgatcaacacgctgaaaag 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726 CCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 aacceteattigaagaagaacgaatgaggaggaceactgiggtgeatgetgattggtteee 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846 AGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCTGCACCACCAACCTAAC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  906 CAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCTCACAGT 965
                                   518 gaaagcotoottggacotootgacogoagtoacaaattgaaactgatoocoagacacacoa 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878 agtggettgececacececttatageatetecetecaggaagetgetgeeaceacetaae 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                               606 GGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                           CACTGTATCCTCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 AACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 cctggatgtgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgca
96.7%; Score 994.4; DB 1; Length 1041; 98.8%; Pred. No. 4.3e-270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Nucleic Acids and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US00/35017A CURRENT FILING DATE: 2000/112-22 PRIOR APPLICATION NUMBER: US09/488,725 PRIOR FILING DATE: 2000-01-21 PRIOR APPLICATION NUMBER: US09/552,317 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 521, Application PC/TUS0035017A GENERAL INFORMATION: APPLICANT: Hyseq Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.8
Matches 1012; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NO FILE REFERENCE: 784PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
PCT-US00-35017A-521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US00-35017A-521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1058 ata 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                       qq
                                                                                                                                                                                                                                                                                                                                   Сp
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

849

784

```
426 CTTCCCTGTCACCGCGAATGTCACTGTGGCCGGCCCATCATTGGCCAGATTATCAAC-C 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephan, Jean-Philippe F. Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 163, Application US/10081056 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
AFPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, P.Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsters, Scot A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 AAAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030 ccaa 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-081-056-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (53)...(40) CTHER INFORMATION: Similar to gil710367 in the genepept database release 114, CTHER INFORMATION: Run with FASTXY 3.3t00, default parameters US-09-471-275-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 agttgacaatactcttaaaaggcatccttgagaaactgaaggtcgacctaggagtgcttca 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 CAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 ACTECTICITICITIC GOOGGOOT GOT CONTROP TO THE TACKTIC TO THE TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 actigiletectytycygegtgeteactyggaeeteagagtetettettgaeatettyg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 CAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 caatgacctaagcaatgtcgtgyataagctggaacctgttcttcacgaggaacttgagac 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 gaaatccagtgcttggcaactggccaagcagaaggcccaggaagctgagaaattgctgaa 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 caaigicattictaagcigcitccaactaacacggacaittitgggilgaaaaicagcaa 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6 CTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTAACCTGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 eteceteateciggatgteaaagetgaacegategatgatgatggeaaagyeettaaeeetgag 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GATTTCATGAGGATCCTCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.78; Score 994.4; DB 18; Length 1041; 98.88; Pred. No. 4.3e-270; Live 0; Mismatches 11; Indels 1;
CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-25
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER APPLICATION NUMBER: US 09/277,490
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \overset{\circ}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
965 TCAGAACAGCAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCCATTTCTGCA 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 cagiggetigececacecettatageatetecetecaggaagetgetgecaceacaa 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910 ccagogigaaagcetgagicocaccagaaggaceticecagaiacectictectictcacag 969
430 cttccctgtcaccgcgaatgtcactgaggccgggcccatcattgaccagattatcaacac 489
                                                                                                                                                                     490 tgagagcoloctlygacoloctgaccycagloacaaltgagactqalocccagacacac 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 tggacaaacacagccaaatcatcaacaagttcgtgaatagcgtgatcaacacgctgaaaa 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 ccctggatgtgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgc 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 AAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCC 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790 aaacceteatetgaagaaggaegaatgaggageaeeactgtggtgeatgetgattggttee 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 CAGTGGCTTGCCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAA 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                905 CCAGCGTGAAAGCCTGAGTCCCACAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAG 964
                                                                                                                                                                                                                                                            545 ACCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGC 604
                                                                                                                                                                                                                                                                                                                                                   550 atcctgttgccggactgggagaalgcgccagagacccaaccagcatctcactttgcttgc 609
                                                                                                                                                                                                                                                                                                                                                                                                                                      605 TGGACAAACACAGCCAAATCATCAAGAGTTCGTGAATAGCGTGATCAACACGCTGAAAA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665 GCACTGTATCCTCCCTGCTGCAGAAGAGATATGTCCACTGATCCGCATCTTCATCCACT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGC 784
                                                                                       485 TGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: 9233591C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
```